

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:56 ; Search time 32.2456 Seconds  
(without alignments)  
800.996 Million cell updates/sec

Title: US-09-826-791A-6

Perfect score: 1768  
Sequence: 1 MERKMSLOPSISVSEMEPN.....KAKTKCVFVSWLAKRETRV 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1779	99.5	346	4	US-09-585-876-2
2	559	31.3	337	3	US-09-044-404A-2
3	559	31.3	337	4	US-09-586-92A-2
4	483.5	27.0	339	1	US-08-153-848-44
5	483.5	27.0	339	2	US-08-812-871-3
6	483.5	27.0	339	3	US-09-299-843A-44
7	483.5	27.0	339	4	US-09-080-337B-44
8	483.5	27.0	339	5	US-09-170-496D-32
9	483.5	27.0	339	5	PCT-US83-11153-44
10	483.5	27.0	339	5	PCT-US95-07180-2
11	480.5	26.9	339	4	US-09-170-496D-182
12	464	25.0	362	3	US-08-513-974B-374
13	447.5	25.0	370	3	US-08-781-250-2
14	446	24.9	373	4	US-09-745-824-14
15	442	24.7	373	2	US-08-559-524A-4
16	442	24.7	373	3	US-08-749-707-4
17	442	24.7	373	4	US-09-947-922-4
18	440	24.6	361	1	US-08-883-750-4
19	440	24.6	361	3	US-08-352-678-4
20	440	24.6	361	4	US-09-356-954-4
21	440	24.6	361	4	US-09-170-496D-78
22	440	24.6	361	4	US-09-829-583B-4
23	440	24.6	361	5	PCT-US93-09636-4
24	439.5	24.6	348	2	US-08-852-824-17
25	439	24.6	302	3	US-08-467-948A-30
26	439	24.6	302	3	US-08-467-947A-30
27	437	24.4	344	2	US-08-467-948A-8

28	437	24.4	344	3	US-08-467-947A-8	Sequence 8, Appl
29	434	24.3	361	4	US-09-170-496D-206	Sequence 206, App
30	434	24.3	377	4	US-09-745-842-17	Sequence 17, Appl
31	424.5	23.7	374	4	US-09-745-842-15	Sequence 15, Appl
32	419.5	23.5	373	3	US-08-513-974B-373	Sequence 373, App
33	419.5	23.5	374	4	US-09-102-710B-3	Sequence 9, Appl
34	416	23.3	342	3	US-08-988-876-9	Sequence 2, Appl
35	416	23.3	375	1	US-08-444-581B-2	Sequence 2, Appl
36	416	23.3	375	1	US-08-446-088A-2	Sequence 2, Appl
37	416	23.3	375	2	US-08-559-524A-3	Sequence 3, Appl
38	416	23.3	375	3	US-08-749-707-3	Sequence 3, Appl
39	416	23.3	375	4	US-09-947-922-3	Sequence 3, Appl
40	409.5	22.9	342	4	US-09-054-272-2	Sequence 2, Appl
41	409.5	22.7	398	1	US-08-097-938-6	Sequence 6, Appl
42	406.5	22.7	398	1	US-08-476-000-6	Sequence 6, Appl
43	406.5	22.7	398	1	US-08-472-840-6	Sequence 6, Appl
44	406.5	22.7	398	1	US-08-476-976-6	Sequence 6, Appl
45	406.5	22.7	398	2	US-08-476-976-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1									
US-09-585-876-2									
Sequence 2, Application US/09585876									
Patent No. 6586205									
GENERAL INFORMATION:									
APPLICANT: Gluckmann, Maria Alexandra									
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like Molecule and									
FILE REFERENCE: 5800-88									
CURRENT APPLICATION NUMBER: US/09/585, 876									
CURRENT FILING DATE: 2000-06-01									
EARLIER APPLICATION NUMBER: 60/182,061									
EARLIER FILING DATE: 2000-02-11									
NUMBER OF SEQ ID NOS: 2									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 2									
LENGTH: 346									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-585-876-2									
Query Match									
Best Local Similarity 99.4%; Pred. No. 3,9e-131;									
Matches 344; Conservative 1; Mismatches 1; Indels 0; Gaps 0;									
QY	1	MERKMSLOPSISVSEMEPNNGTFSNNNSRNCITENFKREFPIVYLIIFFKGLGSLI	60						
DB	1	MERKMSLOPSISVSEMEPNNGTFSNNNSRNCITENFKREFPIVYLIIFFKGLGSLI	60						
QY	61	YVFLPYKSTSVNFMNLAIISDLFTSTLFPADYVIRGSNWIFGDLACRIMSYSLVY	120						
DB	61	YVFLPYKSTSVNFMNLAIISDLFTSTLFPADYVIRGSNWIFGDLACRIMSYSLVY	120						
QY	121	NMYSSIFPLTVLSVVRFLAMVHPRFLHVTISRSAWIIIGIIMIMASSIMLDGSGSQ	180						
DB	121	NMYSSIFPLTVLSVVRFLAMVHPRFLHVTISRSAWIIIGIIMIMASSIMLDGSGSQ	180						
QY	181	NGSVTSCLELNLYKAKLOTMYIALVVGCLLPFFLSICYLIIIRVLAKVEPESGLRV	240						
DB	181	NGSVTSCLELNLYKAKLOTMYIALVVGCLLPFFLSICYLIIIRVLAKVEPESGLRV	240						
QY	241	SHRKALTTIIITLIIIFLCLFPLPYHTLRTHVLTWVKGLCKDRLHKALVTITLAAANACF	300						
DB	241	SHRKALTTIIITLIIIFLCLFPLPYHTLRTHVLTWVKGLCKDRLHKALVTITLAAANACF	300						
QY	301	NPLLYVFAGENFKDRLSALRGHPQAKTKCVFVSWLAKRETRV 346							
DB	301	NPLLYVFAGENFKDRLSALRGHPQAKTKCVFVSWLAKRETRV 346							

```

1  RESULT 2
2  US-09-044-404A-2
3  ; Sequence 2, Application US/09044404A
4  ; Patent No. 6200775
5  ; GENERAL INFORMATION:
6  ; APPLICANT: SATHI, GANESH
7  ; APPLICANT: HALSEY, WENDY
8  ; APPLICANT: ELLIS, CATHERINE
9  ; APPLICANT: AMES, ROBERT
10 ; APPLICANT: FOLEY, JAMES
11 ; APPLICANT: SARAU, HENRY
12 ; TITLE OF INVENTION: CDNA CLONE HMTF81 THAT ENCODES
13 ; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
14 ; NUMBER OF SEQUENCES: 2
15 ; CORRESPONDENCE ADDRESS:
16 ; ADDRESSEE: SmithKline Beecham Corporation
17 ; STREET: 790 Swedeland Road, P.O. Box 1539
18 ; CITY: King of Prussia
19 ; STATE: PA
20 ; COUNTRY: USA
21 ; ZIP: 19406
22 ; COMPUTER READABLE FORM:
23 ; MEDIUM TYPE: Diskette
24 ; COMPUTER: IBM Compatible
25 ; OPERATING SYSTEM: DOS
26 ; SOFTWARE: FastSeq for Windows Version 2.0
27 ; CURRENT APPLICATION DATA:
28 ; APPLICATION NUMBER: US/09/044,404A
29 ; FILING DATE: MARCH 19, 1998
30 ; CLASSIFICATION: 435
31 ; PRIOR APPLICATION DATA:
32 ; APPLICATION NUMBER: 08/844,795
33 ; FILING DATE: APRIL 22, 1997
34 ; ATTORNEY/AGENT INFORMATION:
35 ; NAME: Han, William T.
36 ; REGISTRATION NUMBER: 34,344
37 ; REFERENCE/DOCKET NUMBER: GH-70001-1
38 ; TELECOMMUNICATION INFORMATION:
39 ; TELEPHONE: 610-270-5219
40 ; TELEFAX: 610-270-5090
41 ; TELEX:
42 ; INFORMATION FOR SEQ ID NO: 2:
43 ; SEQUENCE CHARACTERISTICS:
44 ; LENGTH: 337 amino acids
45 ; TYPE: amino acid
46 ; STRANDEDNESS: single
47 ; TOPOLOGY: linear
48 ; MOLECULE TYPE: protein
49 ; US-09-044-404A-2
50
51 Query Match 31.3%; Score 559; DB 3; Length 337;
52 Best local similarity 38.0%; Pred. No.3.8e-36;
53 Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7
54
55 27 NSRNC--TIENKKEFPPIVLLIIFMCGVLNGLSIYFLDPYKSKTSVNVFMLNLATSD 84
56  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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75  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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153 : :
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Db      248 PPHIORTIHLPHLNHETKPCDSVLNMQSGSVITLTLAASNCCEPDLVLFVFGSGNFRKRL- 306
Qy      318 SALRK 322
Db      307 STFRK 311

RESULT 3
US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES U.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTWFB81 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-586-924-2

Query Match      31.3%; Score 559, DB 4; Length 337;
Best Local Similarity 38.0%; Pred. No. 3,8e-36;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

Qy      27 NSRNC--TIENPKKEFPPIVLIIFPGVLGNGLSIVYFLOPKYKSTSVNFMNLAIKD 84
Db      10 SSAATCHPITIDFRNQVYSTLYSMISVVGFGNGSVLVLIKTHYKKAFOYMYMINTLAVD 69
Qy      85 LLIETSLPEFRADYYLKRSGNWIFGDLACRINSYSILYNNMYSIYFLTVLSVFRFLAMWPF 144
Db      70 LLCTCTPLRVRVYVYVHGMIFGDFLCRLSTYALYNALYCSIFPMTAMSFRCIAIVPV 129
Qy      145 RLHVTSGRSAMWILCGIWI-LIWAASSIMLLDSESGNGSVTSCLEINIVKIAK--LQTM 201
Db      130 QNINLVTKKARFVCVGIWIFVILITSSPFLMAKPQKGGKNNTKCEPPODQTKNHVLV 189
Qy      202 NYIALVVGCLLPFETLSICVLLIIRVLLAKYEVDSGHRVSRKALTIITLLIIFPLCL 261
Db      190 HYVSLFVGFIIPFTIILVCTMTIILTLTKSKMKN--LSHKKALIGIMVYTAFLVSPM 247
Qy      262 PYHTRIVVHTTW--KVGCLKD--RLHKAIVITLALAANAACFNPLIYAGENFKORLK 317
Db      248 PYHQRTHLHFLHNETKPCDSVLRMQSGSVITLTLAASNCCEPDLVLFVFGSGNFRKRL- 306
Qy      318 SALRK 322
Db      307 STFRK 311

RESULT 4
US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.

```



```
Sequence 44, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/086,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uni
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.9e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMBPG--TFNNNSRNCTIEN-FKREFPIVYLIIFMGVLGNGLSIYVFLQPYKST 71
DB 5 EVAPPGILTNFSIATACQCGETPLENMLFASFYLLDFILALVNTLALMLFIRDHSGT 64
QY 72 SVNVFMLNLAIISDLFTSLPRADYYLRGSMWIRGDLACRIMSSLSLYNMYSIYFLTV 131
DB 65 PANVFLMLHLAVADISCVLPTRLVYHFGSNHMPFGSICRLNGFLFLYLMNVASISYFLTC 124
QY 133 LSVRFLAMVHPRLLHVTISRSAMWILGIIWILI-MASSIMLLDSSBONGSVTSCLEL 190
DB 125 ISADRFALIVHVPKSLKRRPLVYAHACAFLLWVAVAVAMPPLVSPQTVQTNHTVCLQ- 183
QY 191 NLYKIATLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHR---KALT 247
DB 184 -LYR-EKASHHALVSLAVFTFPFTTTCYLLIIRSL-----RQGLRVERKLTQAVR 235
QY 248 TTIITLILFPLCFGLRYHTLTQTLTKWY--GLCKDRHLKALV--ITLALAAANCPNPL 303
DB 236 MIAIYLAIFLVGVFVHVNRSVYVLHYRSHGASCATORITLALANRITSCITSLNGALDPI 295
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QY 304 LYVFAGENFKDRILKSL-----RKHPQKATK 331
DB 296 MYFFVAEKFRHALCNLLCGRLKGPSPPEGK 327

RESULT 7
US-09-088-337B-44
Sequence 44, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.9e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMBPG--TFNNNSRNCTIEN-FKREFPIVYLIIFMGVLGNGLSIYVFLQPYKST 71
DB 5 EVAPPGILTNFSIATACQCGETPLENMLFASFYLLDFILALVNTLALMLFIRDHSGT 64
QY 72 SVNVFMLNLAIISDLFTSLPRADYYLRGSMWIRGDLACRIMSSLSLYNMYSIYFLTV 131
DB 65 PANVFLMLHLAVADISCVLPTRLVYHFGSNHMPFGSICRLNGFLFLYLMNVASISYFLTC 124
QY 133 LSVRFLAMVHPRLLHVTISRSAMWILGIIWILI-MASSIMLLDSSBONGSVTSCLEL 190
DB 125 ISADRFALIVHVPKSLKRRPLVYAHACAFLLWVAVAVAMPPLVSPQTVQTNHTVCLQ- 183
QY 191 NLYKIATLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHR---KALT 247
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Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVEREKRLTKAVR 235  
Qy 248 TITITLIFPLGLPRLPHHTLRTVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNP 303  
Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCARITLALANRITSCITSLNGALDPI 295  
Qy 304 LYYFAGENFKDRLSKAL-----RKGHPOKAKTK 331  
Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 8  
US-09-170-496D-32  
Sequence 32, Application US/09170496D

GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
TITLE OF INVENTION: Receptor  
FILE REFERENCE: AREN-0040  
CURRENT APPLICATION NUMBER: US/09/170,496D  
CURRENT FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32  
LENGTH: 339  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-170-496D-32

Query Match 27.0%; Score 483.5; DB 4; Length 339;  
Best Local Similarity 34.6%; Pred. No. 2.9e-30;

Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

Qy 16 EMEPRG---TFSPNNNSRNTIEN-FKREPRPIVYLIFPMGVLGNGLSIVFLQPKKST 71  
Db 5 EVAPPEGLITNFSLATVBOCGOETPLENMLFASFYLLDFLTALVGNLTALMLFTRDKSGT 64  
Qy 72 SVNVFMLNLAIDLLFISTLPFRADYLLRGSNMIFGDLACRIMSYSLVYNNMYSIYFLTV 131  
Db 65 PANVFLMHLAVADLSCVLVLPRLVYHBSGNMHPGEIACRLGLFPLYNMASTIYFLTC 124  
Qy 132 LSVFRFLANVHPRRLIHTYSIRSAWILGIIWILI-MASSIMLDGSGSÖNGSVTSCLBL 190  
Db 125 ISADRFIAIVHVKSLKRLRPVLAHLACAFMWVVAVAMAPLLVSPQTVQTNHTVVCLO- 183  
Qy 191 NIYKIAKLOTMYVIALVVGCLLPFTLSICYLLIRVLKVEVPBSGLAVSHR---KALT 247  
Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVEREKRLTKAVR 235  
Qy 248 TITITLIFPLGLPRLPHHTLRTVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNP 303  
Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCARITLALANRITSCITSLNGALDPI 295  
Qy 304 LYYFAGENFKDRLSKAL-----RKGHPOKAKTK 331  
Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 9  
PCT-US93-11153-44  
Sequence 44, Application PC/TUS9311153

GENERAL INFORMATION:  
APPLICANT: Godieka, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schmelkarc, Vicki L.  
TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSES: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11153  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

PCT-US93-11153-44

Query Match 27.0%; Score 483.5; DB 5; Length 339;  
Best Local Similarity 34.6%; Pred. No. 2.9e-30;

Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

Qy 16 EMEPRG---TFSPNNNSRNTIEN-FKREPRPIVYLIFPMGVLGNGLSIVFLQPKKST 71  
Db 5 EVAPPEGLITNFSLATVBOCGOETPLENMLFASFYLLDFLTALVGNLTALMLFTRDKSGT 64  
Qy 72 SVNVFMLNLAIDLLFISTLPFRADYLLRGSNMIFGDLACRIMSYSLVYNNMYSIYFLTV 131  
Db 65 PANVFLMHLAVADLSCVLVLPRLVYHBSGNMHPGEIACRLGLFPLYNMASTIYFLTC 124  
Qy 132 LSVFRFLANVHPRRLIHTYSIRSAWILGIIWILI-MASSIMLDGSGSÖNGSVTSCLBL 190  
Db 125 ISADRFIAIVHVKSLKRLRPVLAHLACAFMWVVAVAMAPLLVSPQTVQTNHTVVCLO- 183  
Qy 191 NIYKIAKLOTMYVIALVVGCLLPFTLSICYLLIRVLKVEVPBSGLAVSHR---KALT 247  
Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVEREKRLTKAVR 235  
Qy 248 TITITLIFPLGLPRLPHHTLRTVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNP 303  
Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCARITLALANRITSCITSLNGALDPI 295  
Qy 304 LYYFAGENFKDRLSKAL-----RKGHPOKAKTK 331  
Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 10  
PCT-US95-07180-2  
Sequence 2, Application PC/TUS9507180

GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: GOCAYNE, JEANINE D  
APPLICANT: ROSEN, STEVEN M.  
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBB69  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```

ADDRESS: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07180-2

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[illegible]

RESULT 11  
 US-09-170-496D-182  
 ; Sequence 182, Application US/09170496D  
 ; Patent No. 6555339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic P.  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Liaw, Chen W.  
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
 ; TITLE OF INVENTION: Receptors  
 ; FILE REFERENCE: AREN-0040  
 ; CURRENT APPLICATION NUMBER: US/09/170,496D  
 ; CURRENT FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 294

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 182
; LENGTH: 339
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-170-496D-182

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Query Match	26.9%;	Score	480.5;	DB	4;	Length	339;
Best Local Similarity	34.6%;	Pred. No.	5e-30;				
Matches	115;	Conservative	62;	Mismatches	130;	Indels	25;
						Gaps	10

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QY      16 EMEPNQ---TFENNNSRCKTEEN-FKREFFPIVYLIIFFMFCVLNGSIIYFLODPYKST  71
Db      5 EVAPPELLINFSLVAEAGCGQETPELLNNLPASFYLLDPFLIALVENTLALMFIIDHSGT  64

QY      72 SVNVFENMLAIAIDDLFIETLPRADYIYLRGSMWIFGDLACIMSYSLYAMYSIYFLTV  133
Db      65 PAWVFLMHLAVADLSCVLLPFLRYLTHSGNMHPGELACLTFGLFYLLNNYASIYFLTC  124

QY      132 LSVVERFLMNVHPFRLIHTYSIRSAWILGIIWILI-MASSIMLDSGSEQSGYSTSCLEL  190
Db      125 ISADRFLLAIIVHVPKSLKLRPLVYAHMLACAFMLVVVAVAMAPLAVSPQTVQGNHTVVCLO-  183

QY      191 NIYTKAKIQTMNYIYALVYGCILPFFYLSICYLLIIRVLLKXVEBSGLRPSHR--KALT  247
Db      184 -LYR-EKSHSHALVSLAVAFTFPFLTYTCYLLIIRSL-----RQGLRVEKRIKLTAKR  235

QY      248 TIIITLIIFFLCDFEYHTLRITVHLITWKK--GLCKDRILKHALV--ITLALAAANACENPL  303
Db      236 MIAIVLAIPLVCFVFEYHVNRSYVYLHVRSHGASCATQRIILANRISCTLSLNGALDPI  295

QY      304 LYVPAGENPCKDRLKSAI-----RKHNQKQAKTK  331
Db      296 MIFVEAKFRNALCNLLCGKRLKGRPPSFSBCK  327

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RESULT 12  
 US-08-513-974B-374  
 Sequence 374, Application US/08513974B  
 Patent No. 6114119  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Maasaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ohnaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiko  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIXE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093969  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:

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1 APPLICATION NUMBER: JP 7-057186
2 FILING DATE: 16-MAR-1995
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: JP 7-007177
5 FILING DATE: 20-JAN-1995
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: JP 6-326611
8 FILING DATE: 28-DEC-1994
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: JP 6-270017
11 FILING DATE: 02-NOV-1994
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: JP 6-236357
14 FILING DATE: 30-SEP-1994
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: JP 6-236356
17 FILING DATE: 30-SEP-1994
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: JP 6-189274
20 FILING DATE: 11-AUG-1994
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: JP 6-189273
23 FILING DATE: 11-AUG-1945
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: JP 6-189272
26 FILING DATE: 11-AUG-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Rebnick, David S.
29 REGISTRATION NUMBER: 34, 235
30 REFERENCE/DOCKET NUMBER: 45753
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 617-523-3400
33 TELEFAX: 617-523-6440
34 INFORMATION FOR SEQ ID NO: 374:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 362 amino acids
37 TYPE: amino acid
38 STRANDEDNESS:
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 OS-08-513-974B-374

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Query Match	26.0%;	Score 464;	DB 3;	Length 362;
Best Local Similarity	30.6%;	Pred. No. 1e-28;		
Matches	99;	Conservative	82;	Mismatches 117; Indels 26; Gaps 7
Qy	16	EMEPNGTSTNNNSRNCTI--ENFKKEFPFIVLIFPFMGVLGNGLSIYVLOPKKSTSV	73	
Db	16	ELLAGGMAGNATKTCSLTKTGFOFYPLTPVYIIVITGFLGNSVAIMIVFHMRWMSG	75	
Qy	74	NVFMNLAIISDLLEFSTLPEFRADYYLRGSNMIFGDLACRIMSYSLYVMYSIPLTVLS	133	
Db	76	SVYMNMLALAPFLYVLTLPALIFYYFNKDWIFGDWCXKLORFIFVNVNIGSILFPTCIS	135	
Qy	134	VVRFLAMVPRFLIVAVTSIRSAMICGIIWIIIMASIMWL---DSGSRQNGSVSCLE-	189	
Db	136	VHRITGVVHPLKSLRKLKKGNVYVSSLWALVAIVAIPILFYSGIVGRNKKIT--CYDI	194	
Qy	190	-----LNLKYIAKIQTMNYIALVWGCLLPFTLSICYLLIRVLLKVEVPSGLRVSHRK	244	
Db	195	TADEXLRSYFVYSMCTVFMFCI-----PFYILGCGYGLVKKALIKYKDLNPSPLR--	246	
Qy	245	ALTTIIITLILIFFLCFPLPYHTLRVYHL-----TTMKVGLCDRLKHALVITLALMAANA	298	
Db	247	STYLIIIVLTVFAVSYLPPHWKKTINLRARLDFOFPQCAFNKVAYATVYTRGLASLNS	306	
Qy	299	CFNPLLYYFAGENFQDRLSALRK	322	
Db	307	CVDPIIVFLAGDTPFRRLRSRATR	330	

```

1 Sequence 2 Application US/08781250
2 Patent No. 6010877
3 GENERAL INFORMATION:
4 APPLICANT: Sathe, Ganesh
5 APPLICANT: Van Horn, Stephanie
6 APPLICANT: Bergsma, Dirk
7 APPLICANT: Mao, Joyce Yue
8 TITLE OF INVENTION: CDNA CLONE HB8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
9 NUMBER OF SEQUENCES: 2
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: SmithKline Beecham
12 STREET: 709 Swedeland Road
13 CITY: King of Prussia
14 STATE: PA
15 COUNTRY: USA
16 ZIP: 19406
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FastSeq for Windows Version 2.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/781,250
24 FILING DATE: 10-JAN-1997
25 CLASSIFICATION: 514
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER:
28 FILING DATE:
29 ATTORNEY/AGENT INFORMATION:
30 NAME: William T. Han,
31 REGISTRATION NUMBER: 34,344
32 REFERENCE/DOCKET NUMBER: ATGS0043
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 610-270-5219
35 TELEFAX: 610-270-4060
36 TELEX:
37 INFORMATION FOR SEQ ID NO: 2:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 370 amino acids
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44 US-08-781-250-2

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Query Match	25.0%	Score 447.5	DB 3	Length 370
Best Local Similarity	31.6%	Prod. No. 2e-27		
Matches 109	Conservative 74	Mismatches 141	Indels 21	Gaps 10
Qy	2	ERKMSLQPSISVSEMEPN-GTFNNNSNRCTI--ENFKKEFPFIYLLIFFPCVGLNGHS	59	
Db	3	DRRIIDQFQDSDNSSLRFLGNATNANT--CIYDDSFKNLNGAVSVFIIIGLITNSVS	60	
Qy	60	IYVFLQPKKTSVNVFMTLAIISDLLFISTLEFRADYYLRGSNMIJGDIACRIMSLSly	119	
Db	61	LPVCFPMKRSRSEFALFITMLAVSDLLFCTLPFKI--FNPNRHPMGDTLCKISTAVL	119	
Qy	120	VNNYSSYIFLTVLSVVRFLMNHPRFLNHTSIRSMILIGIIMILMSSITL-LDSSS	178	
Db	120	TNYGSMFLPTCISVDRFLAIVYPRFSRRIIRTRNSAICAGWILVLSGGISASLFTT	179	
Qy	179	EONGSVTSCLEMLLYKIAK--LOTNMYIALVWGCILPFLTSLICYLLIRVLLKVEPES	236	
Db	180	NNNNATTCGEGSKRWKTYLSKITITFIEVGGFIIPLILNNSCSSVVRITLRK-PATIS	238	
Qy	237	GLNYSHRKATTTIITLIIFFLCFLDHYHTLRVHLLTMMVGLCK--DLNLRALV-ITLA	292	
Db	239	QIGNNKKVLMKLTIMHAAVFVCGFVYNSVLFYLVARSQALTNCLEHFAIMVPTLC	298	
Qy	293	LAAANACFNPILYYFAGENFKD-----RLKSALRKHPQAK	329	
Db	299	IATLNCFCDFPIYFTLSEFQSFYINAHIRMSLSEKTEIPLTTK	343	





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:33 ; Search time 27.1272 Seconds  
(without alignments)  
1227.218 Million cell updates/sec

Title: US-09-826-791a-6

Perfect score: 1788  
Sequence: 1 MERKMSIQPSISVSEMEPN.....KAKTKCVFVSVWLAKITRV 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seque, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	26.3	362	2	S33733 G protein-coupled
2	447.5	25.0	370	2	JCS549 heptahelical p2ys-
3	447	25.0	308	2	I50241 G protein-coupled
4	446	24.9	373	2	JC4737 G protein-coupled
5	442	24.7	373	2	JC4162 p2y receptor - boy
6	440	24.6	361	2	B45680 G protein-coupled
7	436	24.4	344	2	T09508 intron 17 purinerg
8	421.5	23.6	373	2	A47556 ATP receptor p2u -
9	416	23.3	342	2	S13638 placlet-activatin
10	416	23.3	375	2	AS4946 P-2U nucleotide re
11	409.5	22.9	342	2	A40191 placlet-activatin
12	406	22.7	420	2	I51667 chrombin receptor
13	404	22.6	341	2	S63666 placlet activatin
14	400.5	22.4	397	2	S66518 proteinase-activat
15	398	22.3	380	2	I38435 angiotensin recept
16	397	22.2	341	2	S43252 placlet-activatin
17	394.5	22.1	355	2	A45177 chemokine (C-C) re
18	394	22.0	399	2	I48705 proteinase activat
19	393	22.0	355	2	I49339 macrophage inflamm
20	391	21.9	328	2	I55450 G protein-coupled
21	387	21.6	371	2	JCS796 probable chemotr
22	382	21.4	371	2	JCS498 G protein-coupled
23	378	21.2	378	2	B55735 lymphocyte-specifi
24	378	21.1	355	2	UC5067 G protein-coupled
25	377.5	21.1	365	2	S68679 G protein-coupled
26	376	21.0	356	2	I49340 MIP-1 alpha recept
27	374.5	20.9	363	2	I57955 somatostatin recep
28	374.5	20.9	364	2	JN0763 somatostatin recep
29	374.5	20.9	383	2	S55594 G protein-coupled

30	373.5	20.9	387	2	I69202 G protein-coupled
31	372.5	20.8	378	2	A55735 G protein-coupled
32	372	20.8	363	2	I57940 somatostatin recep
33	371.5	20.8	365	2	S68208 G protein-coupled
34	367.5	20.6	427	2	S17148 alpha-chrombin rec
35	366.5	20.5	355	2	G02436 chemokine (C-C) re
36	366	20.5	362	2	JN0694 angiotensin II rec
37	363	20.3	359	2	S15403 angiotensin II rec
38	362.5	20.3	369	2	JC2083 somatostatin recep
39	361.5	20.2	352	2	A43113 chemokine (C-C) re
40	360	20.1	432	2	A43448 chrombin receptor
41	359	20.1	363	2	I48261 angiotensin II rec
42	357	20.0	328	2	JC4800 p2y6 receptor - hu
43	357	20.0	363	2	A49092 angiotensin II rec
44	356.5	19.9	333	2	I65989 G protein-coupled
45	356.5	19.9	361	2	JCS653 G protein-coupled

ALIGNMENTS

RESULT 1  
S33733  
G protein-coupled receptor - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S33733  
R/Webb, T.E.; Simon, J.; Kriehel, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock  
FEBS Lett. 324, 219-225, 1993  
A/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.  
A/Reference number: S33733; MUID:93385340; PMID:8508924  
A/Accession: S33733  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-362 <WEB>  
A/Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CA51716.1; PID:G39508  
A/Superfamily: ATP receptor p2u  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.3%; Score 470; DB 2; Length 362;  
Best Local Similarity 30.6%; Pred. No. 6, 1e-31;  
Matches 99; Conservative 84; Mismatches 115; Indels 26; Gaps 7;

QY	16	EMERNCTSNNSRNCTI--ENFKREFPIYVLIIFPMGVLCNGLSIVFLQPKYSTSV	73
DB	16	ELIAGMAAGNATTCSTKGTGFQFYVLTPTVYIIVITGFGNSVAIMVFHMRWSGI	75
QY	74	NYFMLNLAIISDLFIPTLPFRADYYLRGSMWIFGDLACRIMSYSLVNNYSSIFPLTVS	133
DB	76	SVYMFNLALADPLVYITLPALIFFYFNKTDMIFGDVMTQRFIRVNIYGSILPFTCS	135
QY	134	VVRFLAMVHPRFLHLVTSIRSAMILCGIIMIMASSIML--DSGSBONGSVTSCLE-	189
DB	136	VARYTGVAHPLKSLRKLKQNAVYVSLVAVIAPILFYSGVGRNKTIT-CYDT	194
QY	190	-----LNYKIKLQTMVYIALVVGCLPFFPLSLICYLIIVLVLKVEVPSGLRSHRK	244
DB	195	TADEVYRSFYVSMCTVFMFCI-----PFVILICGYIVKALIKYKDINSPLR---RK	246
QY	245	ATTIIITLIFPLFLPYHTLRTVHL-----TTMKVGLGCDRLHKALVITLAAANA	298
DB	247	SYLVIVITVFAVSYLPRPHVMTLNLRLRDLDPOTPOKCAFNDKYATYATQVTRGLASLNS	306
QY	299	CENPLVYFAGENFDRRLKSALRK	322
DB	307	CVDPIVFLAAGDPFRRLRSRATRK	330

RESULT 2  
JCS549  
heptahelical p2ys-like receptor - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004



P/171-191/Domain: transmembrane #status predicted <TM4>  
P/214-237/Domain: transmembrane #status predicted <TM5>  
P/261-282/Domain: transmembrane #status predicted <TM6>  
P/305-328/Domain: transmembrane #status predicted <TM7>  
P/11-27,113,197/Binding site: carbonyldrate (Aan) (covalent) #status predicted  
P/258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict  
P/330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict  
P/343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depend

Query Match 24.9%; Score 446; DB 2; Length 373;

Best Local Similarity 32.1%; Pred. No. 5.7e-29;

Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY 22 TFSNNNSRNC--TIENFKRFPPIVYLIIFFMGVINGLSIYVFLQPYKKSIVNFMNL 79  
DB 33 TAAVSSSEKCALIKTGFQFYIIPAYIILVFIITGLSNSVALMVFHMKPMGSGISVYMN 92  
QY 80 LAISDLPISTLPFRADYVYLRGSMWIFGDLACRINSYSLYVMYSSIVYLTLSVVRFLA 139  
DB 93 LAAADPLVLTLPALIFVYFNKTDWIFGDAMCKLQRFPHVNLXGSIPLTCLSAHRYSG 152  
QY 140 MVHPRLLHVTISIRSAWILGIIW-ILMASSIMLIDSGS--EQNGSVTSCLE-----L 190  
DB 153 VVYPLKSLGRLLKKKNAICISVLWMLIVVAISPILFVSGTGVKKNKITP-CYDITSDEYL 211  
QY 191 NLXKAKIQTMNYIALVVGCLLPFTLSICYLIIIRVLLKVEVPSGLVSHRKALTTII 250  
DB 212 RSYFIYSMT---TVAMFC-VPLVILIGCYGLIVRALIYKLDNSPLR--RKSIVLYI 263  
QY 251 ITLIIFLCFLPYHTLRVHLTT---WKVGLC--KDLRLKALVITLALAAACFNPL 304  
DB 264 IVLVTPVAVSIFPHWKMKNLRAARDFOFRPMACFNDRYVATYQVTRGLASLNSCVDPL 323  
QY 305 YIFAGEKFKDRKLSALRK 322  
DB 324 YPLAGDTFRRLRSRATRK 341

RESULT 5

JC4162

P2Y receptor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 12-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: J04162

R/Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A/Title: Cloning and characterization of a bovine P2Y receptor.

A/Reference number: J04162; MUID:95352058; PMID:7626079

A/Accession: J04162

A/Molecule type: mRNA

A/Residues: 1-373 <HEN>

A/Cross-references: UNIPROT:P48042; EMBL:X87628; NID:G1032484; PIDN:CAA60958.1; PID:G103

A/Experimental source: aortic endothelial cell

C/Genetics:

A/Gene: bopy2y

C/Superfamily: ATP receptor P2u

C/Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

P/52-77/Domain: transmembrane #status predicted <TM1>

P/88-111/Domain: transmembrane #status predicted <TM2>

P/124-150/Domain: transmembrane #status predicted <TM3>

P/171-191/Domain: transmembrane #status predicted <TM4>

P/214-237/Domain: transmembrane #status predicted <TM5>

P/261-282/Domain: transmembrane #status predicted <TM6>

P/305-328/Domain: transmembrane #status predicted <TM7>

P/11-27,113,197/Binding site: carbonyldrate (Aan) (covalent) #status predicted

P/258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 24.7%; Score 442; DB 2; Length 373;

Best Local Similarity 31.0%; Pred. No. 1.2e-28;

Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

QY 32 TIENFKRFPPIVYLIIFFMGVINGLSIYVFLQPYKKSIVNFMNLAIISDLPISTL 91

DB 45 TKTGFQFYIIPAYIILVFIITGLSNSVALIMVFHMKPMGSGISVYMFNLADFLVLT 104

QY 92 PFRADYVYLRGSMWIFGDLACRINSYSLYVMYSSIVYLTLSVVRFLAHVHPRLLHVT 151

DB 105 PALIIFYFNKTDWIFGDAMCKLQRFPHVNLXGSIPLTCLSAHRYSGVYPLKSGRLK 164

QY 152 IRSAWILGIIWILMASIML---DSGSEONGSVTSCLE-----LNLVYKAKIQTMN 202

DB 165 KKNAYISVLWMLIVVVGSIPLFVSGTGVKKNKITP-CYDITSDEYLASYIYSNCT--- 221

QY 203 YIALVVGCLLPFTLSICYLIIIRVLLKVEVPSGLVSHRKALTTIIITLIIFLCFLP 262

DB 222 --TVAMFC-VPLVILIGCYGLIVRALIYKLDNSPLR--RKSIVLYIILTVFAVSYP 275

QY 263 YHTLRTVHL-----TWKVGCLKDRLLKALVITLALAAACFNPLTYFAGEKFKDL 316

DB 276 FVWKMKNLRAARDFOFRPMACFNDRYVATYQVTRGLASLNSCVDPLIYPLAGDTFRRL 335

QY 317 KSAARK 322

DB 336 SRATRK 341

RESULT 6

B45680

G protein-coupled peptide receptor EBI 2 - human

C/Species: Homo sapiens (man)

C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: B45680

R/Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A/Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A/Reference number: B45680; MUID:93188173; PMID:8383238

A/Accession: B45680

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-361 <BIR>

A/Cross-references: UNIPROT:P32249; GB:L08177; NID:G292056; PIDN:AAA5924.1; PID:G292057

A/Experimental source: B-lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:127096; NCBI:P127097)

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.6%; Score 440; DB 2; Length 361;

Best Local Similarity 32.1%; Pred. No. 1.7e-28;

Matches 102; Conservative 63; Mismatches 135; Indels 18; Gaps 7;

QY 19 PNGTSNNNSRNCITENFKRFPPIVYLIIFFMGVINGLSIYVFLQPYKKSIVNFMNL 78

DB 12 PSATPGNDCCDLYAHNSTARKIYMPRLHSVFIITGLVGNLALVLYONRKKNSTTLVST 71

QY 79 MLASDLPISTLPFRADYVYLRGSMWIFGDLACRINSYSLYVMYSSIVYLTLSVVRFL 138

DB 72 NLVISDILFTTALPFRIVAYAWGFDMRGDALCRITAFVINTYAGVFMTCISIDREI 131

QY 139 AMVHPRLLHVTISIRSAWILGIIWILMASI-MLDSGSEONGSVTSCLE-LNLVYKIA 196

DB 132 AVVHPLARKNKIRISHAGVCFWVILVFAQTLPRLLINPMKQDBERITCMYEPNEETK 191

QY 197 KLQTMNYIALVVGCLLPFTLSICYLIIIRVLLKVE-----VPSGLRVSHRKALTTII 251

DB 192 SLPMILLCFLPYHTLRVHLTTWKVGL-----CKDR--LHKAIVITLALAAACFNPL 248

QY 252 TLIIIFLCFLPYHTLRVHLTTWKVGL-----CKDR--LHKAIVITLALAAACFNPL 304

DB 249 IIVVFLCGTPYHVALIIGHMIK-KLRFNSVFLCQSHSFOISLHFTVCLMNFNCMDPFI 307

QY 305 YIFAGEKFKDRKLSALRK 322

DB 308 YFFACKGYKKRVKRMMLKR 325

RESULT 7

Query Match	24.4%	Score 436;	DB 2;	Length 344;
Best Local Similarity	32.0%	Pred. No. 3.4e-28;		
Matches 98;	Conservative 73;	Mismatches 113;	Indels 22;	Gaps 8;

```

Oy 146 LHVTSIRSAWILCGIWIWILM---ASSIMLDGSEQNGSVTSCHLENLKYIAKQTMN 202
      : : | : | : | : : : | : : : | : : : | : : : | : : : | : : :
Db 124 SKTLRTKRNKAKIVCTGVWLTVIIGGSAIPAVFVOSTHSGNNMSEACFE-NPEPATWTKYLS 182

```

```

QY      203 YIAL---VVGCLLPFFTLSTCYLLIRVLKVEVPESGLRVSHRKALTTITITLIFELC 259
      | : ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
DB      183 RIVAFIEIVCFPIPLINVTCSMWLKTLYR-PVYTSRSKINKTKYLMIFVHLIIFCFQ 241

```

Oy 260 FLPRHTLRVHLTTWKGCLCKDRHKAIV-----ITLALAAANACFNPPLLYYFAGEN 311  
|::|: ::| : : : : | | | : | : | : | : | :  
Db 242 FVPFN----INLLIYSLVRQTFPANCVSVAAVRTMPYTILCAVSNCCFDPIVIYFTSDT 297

Qy	312 FKDRİK 317
	::: !
Db	298 İONSİK 303

RESULT 8  
A47556  
ATP receptor P2u - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: A47556  
R/Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993  
A/Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.  
A/Reference number: A47556; MUID:93281707; PMID:765514  
A/Accession: A47556  
A/Status: preliminary  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-373 <LUS>  
A/Cross-references: UNIPROT:P35383; GB:L14751; NID:G309457; PIDN:AAA39871.1; PID:G309458  
C/Superfamily: ATP receptor P2u  
C/Keywords: transmembrane protein

Query Match	23.6%	Score 421.5	DB 2	Length 373
Best Local Similarity	31.6%	Pred. No. 5.6e-27		
Matches 106; Conservative	69;	Mismatches 131;	Indels 29;	Gaps 10;

```
Oy      15 SEMED-----NGTFSNNN-SRNCIT-ENFKREFPIVLLIFFWGLGNLSIVFLQPY 67
```

Db 3 ADLEPNMSTINGWEDELGKCRFRPDEKRYVLLVSVGVGVCLGLCLNVALYIFLCRL 62

QY 68 KKSTSVNVEFLNLAISDLLFISTLPFRADYLLRGSNMIFGLACRIMSYSLLVNMYSIY 127

Db 63 KTNWASSTYTFHFILAVDSLVAASLPLVLYYVARGHMFPSYVLCKVLEFYTLNYCSIL 122

QY 128 FLVTVSVFRFLAVWHFRLHTVTSIRSAWILGIIWILIMASSIMLL-----DGSGEON 189

Db 123 FLTCISVHRCLGVLRLHSLRWGRARXARVAWVVLVLAQAPVLYFVTSVRGRIT 162

QY 182 GSVTSCLEMLYKIAQLQTMNTIALVVGCL--LPFTLSICYLLIRIVLKEVY--PESGL 238

Db 183 CHDTSARELFHSFVA-----YSSVWLGLFLVAFVPSVILVCYVIMARLLKPAYGTTGL 236

QY 239 RVSHRKALFTIIITIIIFLCFLPHYTLRTVLTATWKGL--CK--DRLHKALVTITLAA 239

Db 237 PRAKRSVRIILVLAVALFCFLPHVYRITLYSPRSADLSCHTLNLINMAKYKTRPLAS 296

QY 296 ANACFNPDLVYFAGENFKRLKSALRKGHQAKT 330

Db 297 ANSCLDPVLYFLAQ---FLVRFAADAKPPTPT 327

RESULT 9  
S13638  
platelet-activating factor receptor - guinea pig  
C,Species: *Cavia porcellus* (guinea pig)  
C,Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C,Accession: S13638

R.Honda, Z. J. Nakamura, M. J. Miki, I. Minami, M. J. Watanabe, T. J. Seyama, Y. J. Okada, H. J. Toh  
 Nature 349, 342-346, 1991  
 Article Cloning by functional expression of platelet-activating factor receptor from guinea pig  
 Reference number: S3638: WUID:91101726: PMID:1446231

A:Accession: S13638  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-342 <HON>

A:Cross-references: UNIPROT:P21556; GB:X56736; NID:949444; PIDD:CAA0060.1;PID:949443  
A:Note: the species of guinea pig is not identified; in Genbank entry CCPAREC, release 3  
C:Superfamily: ATP receptor P2u

Query Match	23.3%	Score 416; DB 2;	Length 342;
Best Local Similarity	30.4%	Pred. No. 1.4e-26;	
Matches 97; Conservative	67;	Mismatches 137;	Indels 18; Gaps 77.

QY 27 NSRNCIENFKREFPIVYLLIFFWGLGNGLSIYF--LQPYKSTSVNFMNLALSD 84  
|| : ||| ||| ||| :: ||| ||| ||| : ||| ||| :: |||  
Db 4 NSSSRVDSEPRYTLFPIVYSIIIFVLGIANGVYLMVPRALYPSSKKNLEIKIFMWLVAD 63

Oy 85 LLPLSTLPRADYYLRGSNNWIFGDLACRIMSYSLYNNVSSLYFLTVLSVVRPLAMVHPF 14  
||| : ||| : : | : | : | : | :  
Db 64 LLPLTLPLMIVVYSNQGNNFLPKFLCNLAGCLFFIITYTCSVAFLGVITYNRFQAVKPI 12

Qy 145 RLHVTIRSAMIICGIIWILIM--ASSIMELD-----SGSEQNGSVTSCLEMLYKIAK 19  
 : : : : : : : : : : : : : : : : : :  
Db 124 KTAQATTTRRGIALSLVIWAIVAAASYFLVMDSTNVVNKACSGNITRCFE-HYEKGSK 18

Qy 198 LQNMVIALVGCCLPFFTUSICYLLIRVLKVEBESGLRVSHRKALTTIIITLIIFP 25  
 : : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 183 PVLIIHICVLGFFIVFELLILFCNLVIITHLRLQPVKQRNAEVRRRALMMVCYLAIVFV 24

Oy 258 LCEPLRYHLTKLVHLLTWKVGICSDRLHKAL-----VITLALAANACFNPBLLYFAGEGNEFK 31  
::|||:: :: :: ||| : | ::| :: :

Dd 243 ICFVRHHNVQ-LRWTLAELGMPPSSNHQAIDANDHQVLCLSLSTNCVDLPVIYCSELTKKFR 30

QY	314	DLKSA	LKRGH	PQAK	TKC	332
				:	:	
Db	302	KHLSEK	---	NIMR	SQKC	317

RESULT 10  
A54946  
P-2U nucleotide receptor - human

RESULT 10  
A54946  
P-2U nucleotide receptor - human

C:\Species: Homo sapiens (man)  
C:\Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1995  
C:\Accession: A54946  
A:\Par: C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A:\Title: Cloning and expression of a human P-2U nucleoside receptor, a target for cystic  
A:\Reference number: A54946; MUID:94211846; PMID:8159738  
A:\Accession: A54946  
A:\Status: Preliminary  
A:\Molecule type: mRNA; protein  
A:\Residues: 1-375 <PAR>  
A:\Cross-references: GB:U07225  
A:\Note: parts of this sequence were confirmed by protein sequencing  
C:\Genetic8:  
A:\Gene: GDB:P2RY2, HP2U, P2U  
A:\Cross-references: GDB:362713; OMIM:60041  
A:\Map position: 11q13.5-11q14.1  
C:\Superfamily: ATP receptor P2u  
C:\Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.3%, Score 416, DB 2, Length 375,  
Best Local Similarity 31.6%, Pred. No. 1.6e-26,  
Matches 100, Conservative 67, Mismatches 131, Indels 18, Gaps 8;

Qy 20 NGTGSNN-SNCTI-ENKREFPPIVYLLIFFGVGLANGSIYFLOPKKTSNVEM 77  
Db 13 NGTWDBELGYRCRPNEDFKYVLLPVSXGVVCLGLCNAAVGLYIFCRLTWNASTYTM 72  
Qy 78 LNLAIIDLPISTPFRADYLLRGSNNWIFGDLACRINSYSLYNMYSIYFLTVLSVRF 137  
Db 73 PHLAVSDALVAASIPLVLYYARQDHPFSTVLCVRFLEYYTMLYCSILPLTICSHRC 132  
Qy 138 LAMVPRLLHTVTSIRSAMILGIIWILIMASSIMELDSGSEQNGSVTSCLEMLYKIAK 197  
Db 133 LGVLRPLRSIRKWRARVARRVAGVAVWLVLACQAPVLYFVTTSAKGLPCTCHDSAPLEFS 192  
Qy 198 LQTMNYIALVVGCL-LPFTLSICILYLLITVLLKVEPES-GRVSHKALTTITITLI 254  
Db 193 -RFAVASYSVMGLLFAVPFAVILVCYVLMARLLKPAVGTSGGLPRAKRSVRTIAVLA 251  
Qy 255 IFFLCSPFPHYTLRTVHJTTWKVGLCKDRHLKALVITLA-----IAANACFPILTYYPAG 309  
Db 252 VFALCFDPFHVTRITLYYSFNSLDL---SCHTLAINMAKYKTVLILASANSCLDPVLYFLAG 308  
Qy 310 ENFDRRLSKALRKGP 325  
Db 309 Q---RLVRPARDAKP 320

RESULT 11  
A40191  
platelet-activating factor receptor - human  
C:\Species: Homo sapiens (man)  
C:\Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:\Accession: A40191, JH0479; A41079; JCI359; A42831; I51923  
A:\Kunz, D.; Gerard, N.P.; Gerard, C.  
J. Biol. Chem. 267, 9101-9106, 1992  
A:\Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell su  
A:\Reference number: A40191, MUID:92250505, PMID:1374385  
A:\Accession: A40191  
A:\Molecule type: mRNA  
A:\Residues: 1-342 <KUN>  
A:\Cross-references: UNIPROT:P25105; GB:M76674; NID:G456293; PID:AAA60002.1; PID:G456294  
R:\Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.  
Biochem. Biophys. Res. Commun. 180, 105-111, 1991  
A:\Title: Characterization of a human cDNA that encodes a functional receptor for platelet  
A:\Reference number: JH0479, MUID:92028922; PMID:1656963  
A:\Accession: JH0479  
A:\Molecule type: mRNA  
A:\Residues: 1-342 <YER>  
A:\Cross-references: GB:M60436; NID:G189537; PID:AAA60001.1; PID:G189538  
A:\Experimental source: granulocyte, cell line HL-60 all  
A:\Nakamura, M.; Honda, Z.; Izumi, T.; Sakenaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Sey

J. Biol. Chem. 266, 20400-20405, 1991

A>Title: Molecular cloning and expression of platelet-activating factor receptor from human platelets  
A:Reference number: A41079; PMID:92041873; PMID:1657923

A:Accession: A41079

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-342 <NA>

A:Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976

R:Szymtomo, T.; Tsuchimochi, H.; McGee, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.

Biochim. Biophys. Res. Commun. 189, 617-624, 1992

A>Title: Molecular cloning and characterization of the platelet-activating factor receptor gene  
A:Reference number: JCI359; PMID:93112021; PMID:1281995

A:Accession: JCI359

A:Molecule type: mRNA

A:Residues: 1-315,'N', 317-342 <STG>

A:Experimental source: heart

A>Note: The authors translated the codon AAT for residue 316 as Lys

R:Seifried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.

Genomics 13, 832-834, 1992

A>Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns &  
A:Reference number: A42831; PMID:92347886; PMID:1322356

A:Accession: A42831

A:Molecule type: DNA

A:Residues: 1-226,'TG', 229-342 <SEV>

A:Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698

A>Note: sequence extracted from NCBI backbone (NCIN:109813, NCIRP:109814)

R:Chase, P.S.; Halonen, M.; Regan, J.W.

Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A>Title: Cloning of a human platelet-activating factor receptor gene: evidence for an intron  
A:Reference number: I51923; PMID:93192035; PMID:8383507

A:Accession: I51923

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-342 <RES>

A:Cross-references: GB:S56396; NID:g298580; PIDN:AAB35755.1; PID:g298581

C:Genetics:

A:Gene: GDB:PTRA

A:Cross-references: GDB:I28806; OMIM:173393

A:Map position: 1p35-1p34.3

C:Superfamily: ATP receptor p2u

C:Keywords: G protein-coupled receptor; transmembrane protein

F:1.7-38/Domain: transmembrane #status predicted <TRI>

F:54-75/Domain: transmembrane #status predicted <TII>

F:92-113/Domain: transmembrane #status predicted <TII>

F:134-155/Domain: transmembrane #status predicted <TVI>

F:184-205/Domain: transmembrane #status predicted <TRV>

F:233-253/Domain: transmembrane #status predicted <TVI>

F:277-297/Domain: transmembrane #status predicted <VII>

QY 304 LYYFAGENFDRRLKSAALRKGHPQAKTKC 332  
 DB 292 IYCFELTKKFR---KHLEKRYSMRSSKRC 317

## RESULT 12

151667  
 thrombin receptor - African clawed frog  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C/Accession: I51667  
 R/Gerstner, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevitz, T.; Turck, C.W.; Vu, T.H.; C  
 Nature 368, 648-651, 1994  
 A/Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac  
 A/Reference number: I51667; MUID:94195429; PMID:8145852  
 A/Accession: I51667  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-420 <GER>  
 A/Cross-references: UNIPROT:P47749; EMBL:U09632; NID:9495197; PIDN:AAA18498.1; PID:94951

Query Match 22.7%; Score 406; DB 2; Length 420;  
 Best Local Similarity 30.9%; Pred. No. 1.2e-25;

Matches 102; Conservative 66; Mismatches 128; Indels 34; Gaps 7;

QY 16 EMBEENGTFSSNNNS-----RNCOTIE-----NFKREFPIVYLIIFFMGVLGNG 57  
 DB 61 ELDESEGGSDQAPVRSARKPRRNTITAEQYLSSQMLTKFVPSIYVFIYVGLPML 120  
 QY 58 LSIYVFLQPYKSTSVNVFNLALISDLLEISTLPFRADYLRGSMWIFGDLACRIMSYA 117  
 DB 121 LAIIIFLPKMKVKKPAVVVWNLALADVPFVSILPKFIATHLGNDMLFGPKCRITVTA 180  
 QY 118 LYNNMTSSYIFLTVLSVRFPLAVNHPRLHNTSISAWLIGIIMILMASSIMLIDSG 177  
 DB 181 FPCNMVCSVLLIASIVDEPLAVVPMHSLSMRTMSRAVWACSFIMLISASTIPPLVTE 240  
 QY 178 SEQ---NGSVTSLLENLKVIALQIMNYIALVVGCL---PEFLTSCYLLIIIRVLK 230  
 DB 241 QYQKIRLDITTHDVLDKDLKDFIYFSSR-CLLFFPVDFITTTICYGIIISLS 298  
 QY 231 VEVPSGLRVSHRKALTTIIITLIFELFPLPYHTLRVHTLTWKVGLCKDRILHKLVT 290  
 DB 299 SSLENS---CKKTRALFLAVVLCVFLICGPTNVFLRHY----LQANEPFYFYIIS 351  
 QY 291 LALAANACGNPLIYFAGENFDRRLKSA 320  
 DB 352 ACVGSVSCCLDPLIYYAASQCQRYLYSIL 381

## RESULT 13

563666  
 platelet activating factor receptor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S63666  
 R/Ishii, S.; Matcunda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.  
 Biochem. J. 314, 671-678, 1996  
 A/Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz  
 A/Reference number: S63666; MUID:962319129; PMID:8670084  
 A/Accession: S63666  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-341 <ISH>  
 A/Cross-references: UNIPROT:Q62035; EMBL:D50872; NID:91256924; PIDN:BAA09468.1; PID:9125  
 C/Superfamily: ATP receptor P2u

Query Match 22.6%; Score 404; DB 2; Length 341;  
 Best Local Similarity 30.5%; Pred. No. 1.4e-25;

Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

QY 17 MBPNGTSSNNNSRNCITENFKREFPIVYLIIFFMGVLGNGLSIYF--LQPYKSTSVN 74  
 DB 17 MBPNGTSSNNNSRNCITENFKREFPIVYLIIFFMGVLGNGLSIYF--LQPYKSTSVN 74

DB 1 MEHNSFRVDS-----EFRYTLFPIYVSIFILGVANGVYLVWVFANLPSPSKLBNIX 53  
 QY 75 VEMNLALISDLLEISTLPFRADYLRGSMWIFGDLACRIMSYLVNMTSSYIFLTVLSV 134  
 DB 54 IFMVLMTADLLFLLTLPIMVIYYNBEQMLPNFLCNVAGCLFFINTYCSVAFGLVITY 113  
 QY 135 VRFPLAVNHPFRLLHNTSISAWILGIIIMILMASSIMLIDSGS-----DONGSVTSC 187  
 DB 114 NKQAVAVIKRQATRRKGLSLIIIVSIVATRSYTLADSTNLPVKNKSGNITTC 173  
 QY 188 LB-LNLKYIAKLQTMNYALVVGCLLPEFTLSICYLLIIRVLKVEVPESGLRVSHRA 245  
 DB 174 FEHYEYVSPIIVNVHFIAF---CFELVFEFLIFPCNLVIHTLLIQPMKQRRKAGVRR 230  
 QY 246 LTTIIITLIFELFPLPYHTLRVHTLTWKVGLCKDRILHKL----VITLALAANACFN 301  
 DB 231 LMMVCTVLAVFLICVPHHVQ-LPWTIAELQY-QTNFQALINDAQITLLSTNCVID 288  
 QY 302 PLIYFAGENFDRRLKSAALRKGHPQAKTKC 332  
 DB 289 PVIYCFELTKKFRKHS---EKRYSMRSSKRC 316

## RESULT 14

566518  
 proteinae-activated receptor 2 precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S66518; S64709; G02131  
 R/Vytedt, S.; Emilsson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.  
 Eur. J. Biochem. 232, 84-89, 1995  
 A/Title: Molecular cloning and functional expression of the gene encoding the human prote  
 A/Reference number: S66518; MUID:96048032; PMID:7556175  
 A/Accession: S66518  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-397 <NYS>

A/Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:91008084; PIDN:CAA90290.1; PID:91008  
 R/Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn,  
 Biochem. J. 314, 1009-1016, 1996  
 A/Title: Molecular cloning, expression and potential functions of the human proteinae-ac  
 A/Reference number: S64709; MUID:96177879; PMID:8615752  
 A/Accession: S64709  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-137; A', 139-397 <BOE>  
 A/Cross-references: EMBL:U34038; NID:91041728; PIDN:AA847871.1; PID:91041729  
 R/Kahn, M.L.; Coughlin, S.R.  
 submitted to the EMBL Data Library, September 1995  
 A/Reference number: H00822  
 A/Accession: G02131  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 29-397 <KAH>  
 A/Cross-references: EMBL:U36753; NID:91208539; PIDN:AAA90957.1; PID:91208540  
 C/Genetics:  
 A/Map position: 5q13  
 A/Introns: 28/1  
 C/Superfamily: ATP receptor P2u  
 F:1-36/Domain: activation peptide #status predicted <APL>  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:37-397/Product: proteinae-activated receptor 2 #status predicted <MAT>

Query Match 22.4%; Score 400.5; DB 2; Length 397;  
 Best Local Similarity 30.7%; Pred. No. 3.1e-25;

Matches 99; Conservative 69; Mismatches 121; Indels 33; Gaps 9;

QY 40 FPPYIYLLIFMGVLGNGLSIYVFLQPYKSTSVNVFNLALISDLLEISTLPFRADYLL 99  
 DB 77 FLPIYIYIVFVGGFSPNSMALWFLFRTKKGPVAVYANALADLSVIFPLIAYHI 136  
 QY 100 RGSNMIFEDDLACRIMSYLVNMTSSYIFLTVLSVRFPLAVNHPRLHNTSISAWILC 159

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Db      137 HGNMNYGALCNVLIGFRYGMNYSILEMTCLSVGRWVIVNPMG----SRKANTAI 192
Qy      160 GI---IWIIMASSIWL-----IDSGEONGSVTSCLENLKYIAKLQTMNY-I 204
Db      193 GISLAIWLLILVTFIPLYVVKQTFIPAL-----NITTCADVLPBQLVGDMEFYPL 244
Qy      205 ALVGC-LRPFTLSICVLLIRVLLKAVPESGLRVSHRKALTTIIITLIIIFLCFLPY 263
Db      245 SLAIGFLEPAFLVMSAVYVLMIRLSSAMDESEK-KRRRAIKLIVTVLAMYLICETPS 303
Qy      264 HTLRFTVHLTVMYGLCKDRHLKALVITLLAAANACFNPFLYYFAGENFKRLKSLRK 323
Db      304 NLLLVHYFLIK-SQGSHVYALXIYALCLSTLNSCIDPEFYIFVSHDFRDAKANLL-- 360
Qy      324 HPQAKTKCVPFVSVWLAKETR 345
Db      361 -CRSVRTVYKQOVSLTSKGR 381
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## RESULT 15

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138435
angiotensin receptor homolog APJ - human
C/Species: Homo sapiens (man)
C/Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C/Accession: I38435
R/O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A/Title: A human gene that shows identity with the gene encoding the angiotensin recepto
A/Reference number: I38435, MUID:94124031, PMID:8294032
A/Accession: I38435
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-380 <RES>
A/Cross-references: UNIPROT:P35414; EMBL:U03642; NID:9425351; PIDN:AAA18954.1; PID:94253
C/Genetics:
A/Map position: 11q12
A/Map position: 11q12
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
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Query Match      22.3%; Score 398; DB 2; Length 380;
Best Local Similarity 29.2%; Pred.No.4.7e-25;
Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;

Qy      17 MEPNGTFSN-----NNSRNCTIENFKRE--FPPIVLIIFFWGVLGNGLSIY-VFLQPYKK 69
Db      1 MREGDGFDMYGGADNGSECEYTDKSSGALIPAIYMLVFLGTGNGLVLMVYFRSRREK 60

Qy      70 STSVNVEMLNLAIIDLFTSTLPFRADYYLRGSNMTFGDLACRIMSYSLVNNYSSIVFL 129
Db      61 RRSADIFIASLAVADLTFTVTLPLMATYTYRDYDMPFGTFPCLSYLIFFVMYASVFCI 120

Qy      130 TILSVVRPLAMHPRPLHVTISRSAMILCGIITIL--IMASSIML-DSGSEONGSVTS 186
Db      121 TGISPDRIYLAIVRPVNAARLRVSGAVATPAVLMLAALLAMPVMLRTTGDELTNTKQ 180

Qy      187 CLELNXYKIAKLQOT-----NMYIALVVGCLLPFTLSICVLLIRVL-----KVEY 233
Db      181 CY-MDSYMAIATVSEWAMEVGLSVSTYGVFPFTIMLTCTYFIAGTIAGHRKERIF- 238

Qy      234 PRSGLRVSHRKALTTIIITLIIIFLCFLPYHTLRVH---LTTWKVGLCKDRHLKALVI 289
Db      239 ---GLR-KRRRLSIIVLVVTFPALCMMPYHLVKTLYMLGSLHWP---CDFDLPLMNIF 291

Qy      290 --TLALAAANACFNPFLYYFAGENFKRLKSLRKHPQAKT 330
Db      292 PYCTCISYVNSCLNPLVAFPDPRFRQACTSMLCCGSRCAGT 334
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Job time : 28.1272 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 20:14:54 ; Search time 205.232 Seconds  
(without alignments)  
8299.718 Million cell updates/sec

Title: US-09-826-791A-5

Perfect score: 1041

Sequence: 1 atgagagaaattatgtc.....gaaggaacaagactataa 1041

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202764 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/pdata/1/1na/5A\_COMB.seq:\*
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  - 3: /cgn2\_6/pdata/1/1na/6A\_COMB.seq:\*
  - 4: /cgn2\_6/pdata/1/1na/6B\_COMB.seq:\*
  - 5: /cgn2\_6/pdata/1/1na/6CTUS\_COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1037.8	99.7	1401	US-09-585-876-1	Sequence 1, Appl
2	145.2	13.9	1578	US-09-044-404A-1	Sequence 1, Appl
3	145.2	13.9	1578	US-09-586-924-1	Sequence 1, Appl
4	99.4	9.5	1020	US-09-170-496D-31	Sequence 31, Appl
5	99.4	9.5	1901	US-09-016-434-1484	Sequence 1484, Ap
6	99.4	9.5	1901	US-08-153-848-43	Sequence 43, Appl
7	99.4	9.5	1901	US-09-299-843A-43	Sequence 43, Appl
8	99.4	9.5	1901	US-09-088-337B-43	Sequence 43, Appl
9	99.4	9.5	1901	PCT-US93-11153-43	Sequence 43, Appl
10	99.4	9.5	2453	PCT-US95-07180-1	Sequence 1, Appl
11	96.2	9.2	1020	US-09-170-496D-181	Sequence 181, App
12	92	8.8	1255	US-08-097-938-3	Sequence 3, Appl
13	92	8.8	1255	US-08-476-000-3	Sequence 3, Appl
14	92	8.8	1255	US-08-476-840-3	Sequence 3, Appl
15	92	8.8	1255	US-08-476-976-3	Sequence 3, Appl
16	92	8.8	1255	US-08-474-410-3	Sequence 3, Appl
17	92	8.8	1255	US-08-486-673B-3	Sequence 3, Appl
18	90	8.6	1224	US-08-742-440A-1	Sequence 1, Appl
19	90	8.6	1414	US-08-476-000-62	Sequence 62, Appl
20	90	8.6	1414	US-08-472-840-62	Sequence 62, Appl
21	90	8.6	1414	US-08-476-976-62	Sequence 62, Appl
22	90	8.6	1414	US-08-474-410-62	Sequence 62, Appl
23	90	8.6	1414	US-08-486-673B-62	Sequence 62, Appl
24	85.6	8.2	1567	US-08-889-108-16	Sequence 16, Appl
25	85.6	8.2	1567	PCT-US94-10358-16	Sequence 16, Appl
26	85.6	8.2	2706	US-08-454-549-1	Sequence 1, Appl
27	85.6	8.2	2706	US-08-454-552-1	Sequence 1, Appl

28	85.2	8.2	1452	1	US-08-149-093A-3	Sequence 3, Appl
29	85.2	8.2	1452	1	US-08-911-245-3	Sequence 3, Appl
30	85.2	8.2	1452	1	US-08-553-058C-3	Sequence 3, Appl
31	85.2	8.2	1452	2	US-08-514-451A-3	Sequence 3, Appl
32	85.2	8.2	1452	3	US-09-170-331-3	Sequence 3, Appl
33	85.2	8.2	1452	3	US-09-510-473-3	Sequence 3, Appl
34	85.2	8.2	1452	3	US-09-048-916B-3	Sequence 3, Appl
35	84.4	8.1	1551	4	US-09-048-434-1239	Sequence 1239, Ap
36	84.4	8.1	1551	4	US-09-023-655-1186	Sequence 1186, Ap
37	84.4	8.1	1780	4	US-09-034-272-1	Sequence 1, Appl
38	83.2	8.0	1098	4	US-09-170-496D-225	Sequence 225, App
39	82.4	7.9	2706	3	US-08-676-351-1	Sequence 1, Appl
40	81.6	7.8	1098	4	US-09-170-496D-117	Sequence 117, App
41	81.6	7.8	1597	2	US-08-724-974A-1	Sequence 1, Appl
42	81.6	7.8	1697	4	US-09-364-425B-26	Sequence 26, Appl
43	81.4	7.8	1164	4	US-09-170-496D-107	Sequence 107, App
44	81.4	7.8	1164	4	US-09-170-496D-221	Sequence 221, App
45	81.4	7.8	2051	4	US-09-016-434-1259	Sequence 1259, Ap

ALIGNMENTS

RESULT 1  
US-09-585-876-1  
Sequence 1, Application US/09585876  
Patent No. 6586205  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria Alexandra  
APPLICANT: Siles-Santiago, Immaculada  
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like Molecule and  
FILE REFERENCE: 5800-88  
CURRENT APPLICATION NUMBER: US/09/565, 876  
CURRENT FILING DATE: 2000-06-01  
EARLIER APPLICATION NUMBER: 60/182,061  
EARLIER FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 1401  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (197) ... (1237)  
US-09-585-876-1  
Query Match 99.7%; Score 1037.8; DB 4; Length 1401;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1039; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGAGAGAAATTTATGTCCTTGCAACCATCATCTCCGTATCAGAAATGAAACCAAT 60  
DB 197 ATGAGAGAAATTTATGTCCTTGCAACCATCATCTCCGTATCAGAAATGAAACCAAT 256  
QY 61 GGCACCTTCAGCAATPACACAGCAGAACTGCACATTTGAAACTTCAAGAGAGATTT 120  
DB 257 GGCACCTTCAGCAATPACACAGCAGAACTGCACATTTGAAACTTCAAGAGAGATTT 316  
QY 121 TTCCCAATTTGATATCTGATATATTTTCTGGGAGCTTGGGAAATGGGTTCCTCA 180  
DB 317 TTCCCAATTTGATATCTGATATATTTTCTGGGAGCTTGGGAAATGGGTTCCTCA 376  
QY 181 TATGTTTCTGACAGCTTATPAGAAGTCCACATCTGTGAAGCTTTTCATGCTTAATCTG 240  
DB 377 TATGTTTCTGACAGCTTATPAGAAGTCCACATCTGTGAAGCTTTTCATGCTTAATCTG 436  
QY 241 GCCATTTAGATCTCTGTTCTTAAGACGCTTCCCTTCAGGCGCTGACTATTAATCTTGA 300  
DB 437 GCCATTTAGATCTCTGTTCTTAAGACGCTTCCCTTCAGGCGCTGACTATTAATCTTGA 496  
QY 301 GGCTCCATTTGATATTTTGAAGACCTGCGCTGACAGATTATCTTATCTTGTATGTC 360

Db 497 GGCCTCAGTTGGATATTTGGAGACCTGGCTGCAGATTAATGCTTAATCTTGTATGTC 556  
Qy 361 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGGCTTCTGGCAATG 420  
Db 557 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGGCTTCTGGCAATG 616  
Qy 421 GTTCACCCCTTTGGGCTTCTGCATGTCCACGATCAGAGGTCCTGGATCCCTGTGGG 480  
Db 617 GTTCACCCCTTTGGGCTTCTGCATGTCCACGATCAGAGGTCCTGGATCCCTGTGGG 676  
Qy 481 ATCATATGATTCCTTAATCATAGGCTTCTCAATAATGCTCCTGACAGTGGCTTGAAG 540  
Db 677 ATCATATGATTCCTTAATCATAGGCTTCTCAATAATGCTCCTGACAGTGGCTTGAAG 736  
Qy 541 AACGCAAGTGTCAATCATATGCTTAAGAGCTGAATCTCTAATAAATGCTAAGCTGACAG 600  
Db 737 AACGCAAGTGTCAATCATATGCTTAAGAGCTGAATCTCTAATAAATGCTAAGCTGACAG 796  
Qy 601 ATGACATATATGCTTGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
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Qy 661 TATCTGCTGATCATTTGGGCTTCTGTTAAAGTGAAGTCCAGAAATCGGGCTGCGGGTT 720  
Db 857 TATCTGCTGATCATTTGGGCTTCTGTTAAAGTGAAGTCCAGAAATCGGGCTGCGGGTT 916  
Qy 721 TCTCACAAGAGGACCTGACACCATCATCATCATCTTATCATCTTCTTGTGTTC 780  
Db 917 TCTCACAAGAGGACCTGACACCATCATCATCATCTTATCATCTTCTTGTGTTC 976  
Qy 781 CTGCCCTATACACATGAGGACCGTCCCTTGAAGCAATGGAATGGGTTAATGCAAA 840  
Db 977 CTGCCCTATACACATGAGGACCGTCCCTTGAAGCAATGGAATGGGTTAATGCAAA 1036  
Qy 841 GACAGACTGATTAAGCTTGTGTTATACACTGAGCTTGGACAGCAATGCTGCTTC 900  
Db 1037 GACAGACTGATTAAGCTTGTGTTATACACTGAGCTTGGACAGCAATGCTGCTTC 1096  
Qy 901 AATCTCTGCTATTAATCTTGTGTTGAGAAATTTTAAAGACAGACTTAAAGTGTGACTC 960  
Db 1097 AATCTCTGCTATTAATCTTGTGTTGAGAAATTTTAAAGACAGACTTAAAGTGTGACTC 1156  
Qy 961 AGAAAAGGCGATCCACAGAAAGGCAAGAAAGTGTGTTCCCTGTGAGTGTGGTTG 1020  
Db 1157 AGAAAAGGCGATCCACAGAAAGGCAAGAAAGTGTGTTCCCTGTGAGTGTGGTTG 1216  
Qy 1021 AGAAAAGGCAAGAGTATTA 1041  
Db 1217 AGAAAAGGCAAGAGTATTA 1237

RESULT 2  
US-09-044-404A-1  
; Sequence 1, Application US/09044404A  
; Patent No. 6200775  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: HALSEY, WENDY  
; APPLICANT: ELLIS, CATHERINE  
; APPLICANT: AMES, ROBERT  
; APPLICANT: FOLEY, JAMES  
; APPLICANT: SARAU, HENRY  
; TITLE OF INVENTION: CDNA CLONE HMTMP1 THAT ENCODES  
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Smithkline Beecham Corporation  
; STREET: 790 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,404A  
FILING DATE: MARCH 19, 1998  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/844,795  
FILING DATE: APRIL 22, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T.  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: GH-70001-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5219  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1578 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-044-404A-1

Query Match 13.9%; Score 145.2; DB 3; Length 1578;  
Best Local Similarity 51.5%; Pred. No. 1.6e-35;  
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;

Qy 93 CACAATTGAAAACCTTCAAGAGAAATTTTCCCAATTGTAATCTGATTAATTTTCTG 152  
Db 514 CACTATTGATGACTTCCGCAATCAAGTATTCACCTGTGCTATGATCTGTGTGT 573  
Qy 153 GGAAGCTTGGGAATGAGGTTGTCAATATGTTTCTCGAGCTTAAAGTCCAC 212  
Db 574 AGGCTTCTTGGCAATGAGTGTGTGCTATGCTCTATTAATAAACCCTATACAGAAAGT 633  
Qy 213 ATCTGTGAACGTTTTCATGCTTAATCTGAGCAATTTCAAGTCTCTGTTCAATAGCAGCT 272  
Db 634 ACCCTTCAAGATATCATGATTAATTTAGAGTACAGATCTACTTGTGTGCACT 693  
Qy 273 TCCCTTCAAGGCTGACTATTAATCTTAAGAGCTTCAATTGATATTTGAGACCTGCTG 332  
Db 694 GCCTCTCGTGTGTCTAATATGATTCACAAAGGCAATTTGGCTTTGTGATCTTGTG 753  
Qy 333 CAGGATTAATGCTTAATCTGATGATGCAACATGACAGCAATTTATTCCTGACCGT 392  
Db 754 CCGCTCAAGACATTAATGCTTGTATGTCACCTCTAATGACATCTTCTTATAGACAC 813  
Qy 393 GCTGAGTGTGTGCTTCTGCAATGATGTTCAACCCCTTGGCTTGTGATGACAG 452  
Db 814 CATGAGCTTTTCCGCTGATGCAATTTGTTTTCAGTCCAGAACATTAATTTGTTTAC 873  
Qy 453 CATCAAGAGTGTGATCTTGTGTGAGTCAATATGATCTT--ATCATGCTTCTC 509  
Db 874 ACAGAAAAGGCAAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933  
Qy 510 AATATGCTCTGAGCAGTGTGCTGACAGAACGAGTGTGACATCATGCTTGAAGT 569  
Db 934 TCCATTTCTTAATGAGCCAAACCAAAAAGATGGGAAAATAATTAACAGTGTGTGAGC 993  
Qy 570 GAATCTTAATAAATGCTAAGCTGCA-----GACCATGAACATTAATGCTTGTGTGT 623  
Db 994 CCAAGAAAGCAATCAAACTTAATAATCATGTTTGTCTGTGATTAATGTCTATTTTGT 1053  
Qy 624 GGGCTGCTGCTGCAATTTTTCACACTGACATCTGTTATCTGCTGATCATTTGGGTTCT 683  
Db 1054 TGGCTTATCATCCCTTTGTATTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1113

QY 684 GTTAAAGTGAAGTCCAGAAATCGGGGCTGGGGTTTCTCACAGAGGCACTGACAC 743  
| | | | |  
DB 1114 ACTAABAAAATCATGAAAATATCTGTCAG-----TCATAAAAGCTATAGAAAT 1167  
| | | | |  
QY 744 CATCATCATACCTTGATCATCTTCTTGTGTGTTCTGCCCCATCACACCTGAGAC 803  
| | | | |  
DB 1168 GATCATGTCGTGACCGCTGCTTTTAACTGATTCATGCAATATCATATCAACGTAC 1227  
| | | | |  
QY 804 CGTCCACTT-----GACGACATGAAAGGCTTTATGCAAGACAGACTGCA 851  
| | | | |  
DB 1228 CATTCACCTTCATTTTTCACAGATGAATAAACCTGTGATTCGTCTTGAATGCA 1287  
| | | | |  
QY 852 TAAAGCTTGTGTTATCACACTGAGCTTGGACAGCAATGCTGCTTCAATCTCTGCT 911  
| | | | |  
DB 1288 GAAGTCCGTGTCATTAACCTTGTCTGCTGCTGATCAATTTGTTGCTTGAACCTCTCT 1347  
| | | | |  
QY 912 CTATTACTTGTGCTGGGAGAAATTTTAAAGACAGACT 947  
| | | | |  
DB 1348 ATATTTCTTTCTGGGGGTAACTTTAGAAAAGGCT 1383  
| | | | |

RESULT 3  
US-09-586-924-1  
; Sequence 1, Application US/09586924  
; Patent No. 6506878  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH M.  
; APPLICANT: HALSEY, WENDY  
; APPLICANT: ELLIS, CATHERINE E.  
; APPLICANT: AMES, ROBERT S.  
; APPLICANT: FOLEY, JAMES J.  
; APPLICANT: SARAU, HENRY M.  
; APPLICANT: CHAMBERS, JON  
; TITLE OF INVENTION: CDNA CLONE HMTMP81 THAT ENCODES A NOVEL  
; FILE REFERENCE: GH-70001-1D1  
; CURRENT APPLICATION NUMBER: US/09/586,924  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: 09/044,404  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 08/844,795  
; PRIOR FILING DATE: 1997-04-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1578  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-586-924-1

Query Match 13.9%; Score 145.2; DB 4; Length 1578;  
Best Local Similarity 51.5%; Pred. No. 1.6e-35;  
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;  
QY 93 CACAAATGAAACTTCAAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTG 152  
| | | | |  
DB 514 CACTATTTGATGACTTCGCAATCAAGTGAATTCACCTGTACTCATATGATCTCTGTGT 573  
| | | | |  
QY 153 GGGAGCTTGGGAAATGGGTTGTCATATATGTTTCTGACAGCTTATAGAAAGTCCAC 212  
| | | | |  
DB 574 AGGCTTCTTGGCAATGGCTTTGTGCTCATATGCTCATATAAACTATCAAGAAAGTC 633  
| | | | |  
QY 213 ATCTGTGAACGTTTCAATGCTAAATCTGGCAATTCAGATCTCTGTTCATAAGACGCT 272  
| | | | |  
DB 634 AGGCTTCAAGTATACATGATTAATTTAGAGATGAGATCTACTTGTGTGACACACT 693  
| | | | |  
QY 273 TCCCTTCAAGGCTGATATATCTTAGAGGCTCAATGATATTTAGAGAACTGGGCTG 332  
| | | | |  
DB 694 GCTCTCCGTGTCATATATGTCACAAAGGCAATTTGGCTCTTGGAGACTTCTTGTG 753  
| | | | |  
QY 333 CAGAGTATATGTTATTTCTTGTATGTCACATGATGACAGATATTTATTTCTGACCGT 392  
| | | | |  
DB 754 CGGCTTCAGACCTATGCTTTGTATATGTCACATCTCATATGACATCTTCTTATGACAGC 813  
| | | | |

QY 393 GCTGAGTGTGTCGCTTCTGGAATGTTCAACCCCTTTCGGCTTCTGATGACACAG 452  
| | | | |  
DB 814 CATGAGCTTTTCCGCTGATGCAATGTTTTCAGTCCAGAACATTAATTTGGTTAC 873  
| | | | |  
QY 453 CATCAGAGTGTGCTGATCTCTGTGGGATCATATGATCTCT--ATCATGCTTCTTC 509  
| | | | |  
DB 874 ACAGAAAAAGCCAGGTTGTGTGTGATGATTTGGAATTTTGTGATTTTGAACCACTTC 933  
| | | | |  
QY 510 AATATATGCTCTGACAGTGGCTCTGAGCAGAAACGCACTGTCATCATATGCTTGAAGCT 569  
| | | | |  
DB 934 TCCATTTCTTAATGGCCAAACCAAAAAGATGGAAAAATTAACCAAGCTTGGAGCC 993  
| | | | |  
QY 570 GAATCTTATTAATTAATTTCTAGCTGCA-----GACATGAATCATATATGCTTGGTGT 623  
| | | | |  
DB 994 CCCAAGACATTCAAATCTAAATATCATGTTTGTGCTTGCATATATGTCATTTGTTGT 1053  
| | | | |  
QY 624 GGGCTGCTGCTGCAATTTTTCACACTGACATCTGTATCTGCTGATCATTTGGGTTCT 683  
| | | | |  
DB 1054 TGGCTTTATCATCCCTTTTGTATATATGTCGTGTTACAAATGATCATTTTGAACCTT 1113  
| | | | |  
QY 684 GTTAAAGTGAAGTCCAGAAATCGGGGCTGGGGTTTCTCACAGAGGCACTGACAC 743  
| | | | |  
DB 1114 ACTAABAAAATCATGAAAATATCTGTCAG-----TCATAAAAGCTATAGAAAT 1167  
| | | | |  
QY 744 CATCATCATACCTTGATCATCTTCTTGTGTGTTCTGCCCCATCACACCTGAGAC 803  
| | | | |  
DB 1168 GATCATGTCGTGACCGCTGCTTTTAACTGATTCATGCAATATCATATCAACGTAC 1227  
| | | | |  
QY 804 CGTCCACTT-----GACGACATGAAAGGCTTTATGCAAGACAGACTGCA 851  
| | | | |  
DB 1228 CATTCACCTTCATTTTTCACAGATGAATAAACCTGTGATTCGTCTTGAATGCA 1287  
| | | | |  
QY 852 TAAAGCTTGTGTTATCACACTGAGCTTGGACAGCAATGCTGCTTCAATCTCTGCT 911  
| | | | |  
DB 1288 GAAGTCCGTGTCATTAACCTTGTCTGCTGCTGATCAATTTGTTGCTTGAACCTCTCT 1347  
| | | | |  
QY 912 CTATTACTTGTGCTGGGAGAAATTTTAAAGACAGACT 947  
| | | | |  
DB 1348 ATATTTCTTTCTGGGGGTAACTTTAGAAAAGGCT 1383  
| | | | |

RESULT 4  
US-09-170-496D-31  
; Sequence 31, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-170-496D-31

Query Match 9.5%; Score 99.4; DB 4; Length 1020;  
Best Local Similarity 48.8%; Pred. No. 5.3e-21;  
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;  
QY 119 TTTTCCCAATTTGATATCTGATTAATATTTTCTGGGAGATCTTGGGAAATGGTGTCCA 178  
| | | | |  
DB 98 TGTTCGCTCCCTTCACTTCACTTGGATTTATCTCTGCTTTAGTGCATTAACCTGAGCTC 157  
| | | | |  
QY 179 TATATGTTTCTGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATC 238  
| | | | |

Db	158	TGAGGCTTTTCATTCGAGACACAAAGTCGGAGACCCCGGCAAGTGTCCTGATGATC	21.7
Qy	239	TGGCATTTCAGATCTCTGTTCTATAGACCGCTTCCTTAGGGCTACTATATATCTTA	238
Db	218	TGGCCGGGGCCGACTTGTCGTGTGTGCTGGATCTCTGCCACCGCCTGTGATCAACTTCT	27.7
Qy	299	GAGGCTCCAAATTGATATTTTGGAGACTGGCTGGAGGATTAATGCTTAATCTTGATG	35.8
Db	278	CTGGGAACCACTGGCCATTTTGGGGAATGCAATGCCGTCTCAACGGGCTTCTCTTCAAC	33.7
Qy	359	TCAACATGTAACAGCACTATTTATTTCTGACCGGTGCTGAGTGTGTGCTTCTGGCAA	41.8
Db	338	TCAACATGTAACGACCACTACTCTTCTCACTCCATGATCAGGCGGACCGTTTCTGGCCA	39.7
Qy	419	TGGTTCAACCCCTTTCGGCTTCTGCACTGTACACAGATAGAAGTGTCTGATCTCTGTG	47.8
Db	398	TTGTGACACCGGGTCMAAGTCCCTCAAGCTCCGACGGCCCTCTACGCACACCTGGCTGTG	45.7
Qy	479	GGATCATATGATCCTTATCATAGGCTTCCTCAATATAGTCTCTGGAAGTGGCTCTAGC	53.8
Db	458	CTTTCCTGAGGGTGTGTGTGTGCTGTGGCCATGGCCCGCCGTGTGTGAGCCACAGACG	51.7
Qy	539	AGAACGGCAGTGTACATCATCTTAAAGCTGAATCTCTATAAATTTCTAAGCTGACGA	59.8
Db	518	TGCAAGACCAACCAACGAGTGATCTGTCTGTGCACTTACCGGAGAAAGCCTCCACATG	57.7
Qy	599	CCATGAATATATATGCTCTGGTGTGTGTGGCTGTGCTGTGCACTTTTCACTACGACAT	65.8
Db	578	CCCTGG-----TGCTCTGGACAGTGTGGCTTACCTCCCGTTCATCAACGGTCACT	63.1
Qy	659	GTTATCGCTGATCATTCGGGTTCTGTTAAAGTGAAGTCCCAATCCGAGGCGTGGGG	71.8
Db	632	GCTACCTGCTGATCATCCGAGCTGTGGCAAGGCTCTGTGTGAAGAAAGGCTCTCAAG-	69.0
Qy	719	TTTCTCAAGAAAGGACTGACCAACATCATCATCACTTGATCATCTTCTTGTGT	77.8
Db	691	-----ACCAAGGAGTGTGGCATGTGCTGCAATGCTGTGCTCTTCTGTGTGCT	74.2
Qy	779	TCCTGCCCTATACACACTGAGAGCCGTCACATTG	81.3
Db	743	TCGTGCCCTACACGTCACACCGCTCGTCTACGTG	77.7
RESULT 5			
US-09-016-434-1484			
/ Sequence 1484, Application US/09016434			
/ Patent No. 6500938			
GENERAL INFORMATION:			
APPLICANT: Janice Au-Young			
APPLICANT: Jeffrey J. Seilhamer			
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING			
TITLE OF INVENTION: PATHWAY GENE EXPRESSION			
NUMBER OF SEQUENCES: 1490			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.			
STREET: 3174 PORTER DRIVE			
CITY: PALO ALTO			
STATE: CALIFORNIA			
COUNTRY: USA			
ZIP: 94304			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/016,434			
CLASSIFICATION:			
FILING DATE: HEREWITH			
PRIORITY APPLICATION DATA:			
APPLICATION NUMBER:			
FILING DATE:			
CLASSIFICATION:			

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Zeller, Karen J.
: REGISTRATION NUMBER: 37,071
: REFERENCE/DOCKET NUMBER: PA-0002 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 845-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 1484:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1900 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GENBANK
: CLONE: g992699
: US-09-016-434-1484

Query Match          9.5%; Score 99.4; DB 4; Length 1900;
Best Local Similarity 48.8%; Pred. No. 8e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

QY      119  TTTTCCCAATGTATATCTGATTAATATTTTTCTGGGAGTCTTGGAATGGGTGTGCA 178
Db      797  TGTTCGCTCCTTCTTACCTTCTGGATTTTATCTGGCTTTAGTTGGCAATACCTGCTC 856

QY      179  TATATGTTTTCTCGACGCTTATAAGAGTCCACATCTGGAAGCTTTTCACTGTAATC 238
Db      857  TGTGCTTTTTCATCTCGAGACCAAGTCCGGGACCCCGGCCAAGTGTCTGTATGATC 916

QY      239  TGGCATTTTACAGATCTCCTGTTCATTAAGCAAGCTTCCTTCAGGAGTCACTATTATCTA 298
Db      917  TGGCCGTGGCCGACTTGTCTGTCTGCTGCTGCTGCTGCCAACCCTGTGTCAACATCTT 976

QY      299  GAGGCTCCAAATTGGATATTGGAAGACCTGGGCTGACAGATTAATGTTTATCTTGTATG 358
Db      977  CTGGGAACCACTGGCCATTTGGGGAATCGATGCGGTCTACCGGGCTTCTTTTACC 1036

QY      1037  TCACATAGTACGCGAGATCTTACTTCTCACCTGCATCAGGCGGACCGTGTCTTGCGCA 1096
Db      419  TGTGTACACCCCTTTCGGCTTCTGATGTCAACAGACATCAGGAAGTCCGTGATCCTGTG 478

QY      1097  TTGTGACACCGGCTCAAGTCCCTCAAGCTTCGAGAGCCCTCTTACGACACCTGGCTGTG 1156
Db      479  GGATCATATGGATCCTTATCATATGAGCTTCTCAATAATATGCTCTGGAAGTGGCTGTAGC 538

QY      1157  CTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1216
Db      539  AGAAGCGCAGTGCATCATATGCTTTAAGCTGAATCTCTATAAATTTGCTAAGTGCAGA 598

QY      1217  TGCAGACCAACCAACAGGTGTGTGCTGTGAGCTGTACCGGGAGAAAGGCTCCACCATG 1276
Db      599  CCATGAATATATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 658

QY      1277  CCGTGG-----TGTCCCTGTGCAATGGCCCTTCACTTCCGTTCATCAACAGGTCACT 1330
Db      659  GTTATCTGCTGATGATTCGGGTTCTGTAAAGTGAGAGTCCAGAAATCGGGGCTGCGGG 718

QY      1331  GCTACTGTGTGATATCCGAGCCTGTGGGACGGGCTTCGTGTGAAGAGGCTTCAAG- 1388
Db      719  TTTTCTCAGGAAGGCACTGACCAACCATCATCATCATCTTGATCATCTTCTTGTGTGTT 778

QY      1390  -----ACCAAGGCAGTGGGATGATGCGCAATAGTGTGGCATCTTCTGTGTGTGCT 1441
Db      779  TCTGTCCCTTATCACACCTAGAGCGGTCCAATTG 813

QY      1442  TCGTGCCCTTACCAAGTCAACCGCTCCGTTCACGTG 1476
Db      779  TCTGTCCCTTATCACACCTAGAGCGGTCCAATTG 813

RESULT 6
US-08-153-948-43

```



SEQUENCE CHARACTERISTICS:  
LENGTH: 1901 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 701..1717  
US-09-299-843A-43

Query Match 9.5%; Score 99.4; DB 3; Length 1901;  
Best Local Similarity 48.8%; Pred. No. 8e-21;  
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

119 TTTTCCCAATTGATATCTGATATATATTTCTGGGAGCTTGGGAATGGGTTGCCA 178  
798 TGTTCGCTCTCTTACCTTCTGATTTTATCTGGCTTAGTTGGCAATACCTGGCTC 857  
179 TATATGTTTCTGACGCTTATTAAGATCCACATCTGNAAGCTTTGATGCTAAATC 238  
858 TGTGCTTTTCAATCCGAGACCAAGTCCGGACCCCGCAACGTTTCTGATGATC 917  
239 TGGCCATTTGAGATCTCTGTTCAATAGACAGCTTCCCTTCAGAGCTGATATATCTTA 298  
918 TGGCCGTGGCGCACTGTGTGTGTGTGTCTGCTGCCACCGCTGTGTACCACTTCT 977  
299 GAGGCTCCATTTGATATTTTGGAGACCTGGCTTCGAGATTAATGTTCTTATCTTGTATG 358  
978 CTGGGAACCACTGCGCATTTGGGGAATCGCAATGCGCTTCACCGGCTTCTCTTACCC 1037  
359 TCAACATGATACAGATATTTATTTCTGACGCTGCTGAGTGTGTGCGTTTCTGGCAA 418  
1038 TCAACATGATACAGATATTTATTTCTGACGCTGCTGAGTGTGTGCGTTTCTGGCAA 1097  
419 TGGTTACCCCTTTGGGCTTCTGATGTCAACAGATCAGAGTGGCTGATCTCTGTG 478  
1098 TTGTGCAACCGGTCAGATCCCTCAAGCTCGGAGGCCCTCTACGACACCTGGCTGTG 1157  
479 GGATCATATGATATCTTATCATATGCTTCTCAATATATGCTCTGAGACATGGCTCTGAGC 538  
1158 CCTTCTGTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1217  
539 AGAAGCGAGATGATCATATGCTTAGAGCTGAATCTTATAAATTTGCTAAGCTGAGA 598  
1218 TGAAGACCAACCAACGATGCTGTGCTGACGCTGACGAGGAGAGGCTCTCCACCAATG 1277  
599 CCATGATATATATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 658  
1278 CCTGG-----TGTCCGTGGAGTGGCTTCACTTCCGTTCAATACCAAGGTACCT 1331  
659 GTTATGCTGATATCTGAGGCTTCTGATTAAGATGAGATCCCAAGATGGGGCTGGGG 718  
1332 GCTACCTGTGATCATCCGAGCTTGGGAGGGCTGGGTGTGGAAGAGCCCTCAAG- 1390  
719 TTTCTCAGAGAGGACATGACCAACCATCATATCACTTGAATCATCTTCTTGTGTT 778  
1391 -----ACCAAGGAGTGGCATATGCTGATGCTGCTGCTTCTTCTGTGCT 1442  
779 TCTGCTCATATCAACATGAGAGCGTCACTTG 813  
1443 TGTGCTTACCAACGTCACCGCTCGTCTACGTG 1477

## RESULT 8

US-09-088-337B-43  
Sequence 43, Application US/09088337B  
Patent No. 6348574

## GENERAL INFORMATION:

APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Born  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:

NAME: No. 6348574and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1901 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:

NAME/KEY: CDS  
LOCATION: 701..1717  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-088-337B-43

Query Match 9.5%; Score 99.4; DB 3; Length 1901;  
Best Local Similarity 48.8%; Pred. No. 8e-21;  
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

119 TTTTCCCAATTGATATCTGATATATTTCTGGGAGCTTGGGAATGGGTTGCCA 178  
798 TGTTCGCTCTCTTACCTTCTGATTTTATCTGCTTGTAGTTGGCAATACCTGGCTC 857  
179 TATATGTTTCTGACGCTTATTAAGATCCACATCTGTAAGCTTTTCAATGCTAAATC 238  
858 TGTGCTTTTCAATCCGAGACCAAGTCCGGAGCCCGCAACGTTTCTGATGATC 917  
239 TGGCATTTGAGATCTCTGTTCAATAGACAGCTTCCCTTGAAGGCTGACATATATCTTA 298  
918 TGGCGTGGCGCATGTCGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977  
299 GAGGCTCAATTGATATTTGAGACCTGGCTGAGAGATTAATGCTTATCTTGTATG 358  
978 CTGGGAACCACTGGCATTTGGGGAATCGATGCGTCTACCGGCTTCTCTTACCC 1037  
359 TCAACATGATACAGATATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAA 418  
1038 TCAACATGATACAGATATTTATTTCTGACCTGATCAAGGCGGACCGTTTCTGGCAA 1097  
419 TGTTCACCCCTTTGGGCTTGTGATGTCAACAGATCAAGAGTGGCTGATCTCTGTG 478  
1098 TTGTGCAACCGGTCAGATCCCTCAAGCTCGGAGGCCCTCTTACGACACCTGGCTGTG 1157  
479 GGATCATATGATCTTATCATATGCTTCTCAATATATGCTCTGGAACAGTGGCTCTGAGC 538

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Db      1158 CCTTCTGTGGGTGGTGGTGGTGGCCATGAGCCCCGCTGCTGGTGAACCCACAGACCG 1217
Qy      539 AGAAGCGGAGTGTCAATCATGCTTAGAGCTGAATCTTATTAATTTGCTTAGAGTCAGAG 598
Db      1218 TGCAGACCAACCAACGAGTGTGCTGCTGACGTGACCGGAGAGGCGCTCCACCATAG 1277
Qy      599 CCATGAACATATTTGCTGTGTGGTGGGCTGCTGCTGTCATTTTTCACATTCAGATCT 658
Db      1278 CCTGG-----TGTCCCTGGAGTGGCCCTTCACCTTCCGTTCAACACGCTACCT 1331
Qy      659 GTTATCTGTGATCATCTCGGGTTCTGTAAAGTGAAGGTCCAGAAATCGAGGCTGCGGG 718
Db      1332 GGTACTGTGTATCATCCGACGCTGCGGAGGCGCTGCTGTGAAGAGTCCCTCAAG- 1390
Qy      719 TTTCTCAGAGAGGCACTGACCAACCATCATCATCACTTGAATCATCTTCTTGTGT 778
Db      1391 -----ACCAAGGAGAGTGCATATGTCATAGTGTGGCCATCTTCTGTGTGCT 1442
Qy      779 TCTGCCCCATGACACACGTGAGGACCGTCCACTTG 813
Db      1443 TGTGCCCCAACAAGTCAACCGCTCCGTACGTG 1477

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## RESULT 9

```

PCT-US93-1153-43
/ Sequence 43, Application PC/TUS9311153
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schwellhart, Vicki L.
/ TITLE OF INVENTION: Novel Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 64
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSER: Bicknell
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/11153
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Noland, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1901 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 701..1717
/ PCT-US93-1153-43

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Query Match 9.5%; Score 99.4; DB 5; Length 1901;  
 Best Local Similarity 48.8%; Pred. No. 86-21;  
 Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

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Qy      119 TTTTCCCAATTTGATATCTGATATATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCA 178
Db      798 TGTTCGCTCCTTTACCTTCTGATATTTATCTGTGGCTTTAGTTGGCAATACCTGTGCTC 857
Qy      179 TATATGTTTCTGTGACCTTTAAGAAAGTCCACATCTGTGAACGTTTCAATGCTAATG 238
Db      858 TGTGTCTTTTCAATCCGAGACCAAGTCCGGAGACCCCGGCAACGTTTCTGATGCAATC 917
Qy      239 TGGCCATTTCAATCCTCGTTGATATAGACAGCTTCCCTTGAGGGGTGACTATTAATCTTA 298
Db      918 TGGCCGTGGCCGACTTGTGTGTGCTGTGCTGTCTTCCACCCGCTGTGTACATCTTCT 977
Qy      299 GAGGCTCCAAATTTGATATTTGAGACCTGGCCCTGAGAGATTAATGTTTATTCCTTGTATG 358
Db      978 CTGGGAACCACTGGGCATTTGGGGAATGCGATGCGCTCAACCGGCTTCTCTTAC 1037
Qy      359 TCAACATGTACAGCAATTTATTTCTGTGACCGCTGTAGTGTGTGCGTTTCTTGGCAA 418
Db      1038 TCACATGTACCGCAGCATCTTCTTCACTGTGATCGCCGACCGCTTTCTTGGCCA 1097
Qy      419 TGGTTACCCCTTTGGGCTTGTGACATGTACAGCATGAGAGTGCCTGATCCTGTG 478
Db      1098 TTGTGACCCGCTCAAGTCCCTCAAGCTCCGAGGCGCTTCAACGACACTGGCTGTG 1157
Qy      479 GGATCATATGATTCCTTATCATAGGCTTCTCTCAATATGCTCTCTGACAGTGGCTGTGAGC 538
Db      1158 CCTTCTGTGGTGTGGTGGTGTGGCCATGAGCCCGCTGTGTGGAGCCCAAGACCG 1217
Qy      539 AGAAGCGGAGTGTCAATCATGCTTAGAGCTAATCTTATTAATTTGCTTAAGCTGACAG 598
Db      1218 TGCAGACCAACCAACGAGTGTGCTCTGCACTGACCTGAGACCGGAGAGGCTCCACCATAG 1277
Qy      599 CCATGAACATATTTGCTGTGTGGTGGGCTGCTGCTGTCATTTTTCACACTCAGATCT 658
Db      1278 CCTGG-----TGTCCCTGGAGTGGCCCTTACCTTCCGTTCAACACAGGTACCT 1331
Qy      659 GTTATCTGTGATCATCTCGGGTTCTGTAAAGTGAAGGTCCAGAAATCGAGGCTGCGGG 718
Db      1332 GGTACTGTGTATCATCCGACGCTGCGGAGGCGCTGCTGTGAAGAGCGGCTCAAG- 1390
Qy      719 TTTCTCAGAGAGGCACTGACCAACCATCATCATCACTTGAATCATCTTCTTGTGT 778
Db      1391 -----ACCAAGGAGAGTGCATATGTCATAGTGTGGCCATCTTCTGTGTGCT 1442
Qy      779 TCTGCCCCATGACACACGTGAGGACCGTCCACTTG 813
Db      1443 TGTGCCCCAACAAGTCAACCGCTCCGTACGTG 1477

```

## RESULT 10

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PCT-US95-07180-1
/ Sequence 1, Application PC/TUS9507180
/ GENERAL INFORMATION:
/ APPLICANT: LI, YI
/ APPLICANT: GOCAYNE, JEANINE D
/ APPLICANT: RUBEN, STEVEN M
/ TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBBB69
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN, CECCHI,
/ ADDRESSER: STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patent In Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: PCT/US95/07180
:
: FILING DATE: 06-JUNE-1995
:
: CLASSIFICATION:
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: MULLINS, J.G.
:
: REGISTRATION NUMBER: 30,073
:
: REFERENCE/DOCKET NUMBER: 325800-366
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 201-994-1700
:
: TELEFAX: 201-994-1744
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 2453 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: DNA (genomic)
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: 548..1564
:
: PCT-US95-07180-1

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Query Match	9.5%;	Score 99.4;	DB 5;	length 2453;
Beet Local Similarity	48.8%;	Pred. No. 9.5e-21;		
Matches 339;	Conservative 0;	Mismatch 341;	Indels 15;	Gaps 2;
Qy	119	TTTTCCCAATGTATATCTGATATATATTTTTCTGGGGAGCTTTGGGAAATGGGTGTGCA	178	
Db	645	TGTTGGCCCTCTTACCTCTTGATTTTATCTGGCTTTAAGTGGCAATACCTTGCTC	704	
Qy	179	TATAGTTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAAGCTTTTACGTCTAAATC	238	
Db	705	TGTGGCTTTTATCGAGAACCAAGAGTCCGGGACCCCGGACCAAGCTGTCTTCGATGATC	764	
Qy	239	TGGCATTTCAGATCTCCGTGTTTCATTAAGACAGCTTCCCTTGAAGGGCTACATTAATCTTA	298	
Db	765	TGGCGTGGCGGACTTGTGTCGTCGTGCTCTCCACCGCGCTGTCTTACCACTTCT	824	
Qy	299	GAGGCTCCAAATTGATATTTTGGAGACCTGGCCCTGGAGATTATGTCTTATTCCTGTATG	358	
Db	825	CTGGAAACACCTGGGCAATTTGGGGAAATCGATGCGCTTCACCGGCTTCTCTTAC	884	
Qy	359	TCAACATGTACAGCAGTATTTATTTCCGACCGGTGAGTGTGTGGCTTTCTGGCA	418	
Db	885	TCAACATGTACAGCAGTATTTATTTCTCACCTGTGATAGGCGGACGTTTCTTGCGCA	944	
Qy	419	TGTTTACCCCTTTGCGCTTCGTGATGTACACAGATCAGAGAGTCCGTCTGTG	478	
Db	945	TTGTGACCCCGGTCAAGTCCCTCAAGCTCCGAGAGGCCCTGTAGCAACCTGGCCGTG	1004	
Qy	479	GGATCATATGGAATCCTTATCATAGCTTCCTCAATAATAGTCTCTGGACAGTGGCTTAAC	538	
Db	1005	CTTTCCTGTGGGTGTGGTGGCTGTGGCATAGCCCCGCTGTGTGAGCCACAGACG	1064	
Qy	539	AGAAAGGAGTGCATCATGCTTTAAGCTGAATCTCTATAAATGTTCTAAGCTGAGA	598	
Db	1065	TGCAGACCAACCAACAGGTGGTGTGCGTGAGCGTATACCGGAGAAAGCCCTCCACATG	1124	
Qy	599	CCATGAATATATGCTGTGTGTGGTGGCTGCTGGCCATTTTTCACACTGACATCT	658	
Db	1125	CCCTGG-----TGTCCCTGGCAATGGCTTTCACCTTCCGTTTCATACCAAGGTACCT	1178	
Qy	659	GTTATCTGTGATCATTTGCGGTTTGTGTTAAAGTGAAGTCCAGAAATCGGGGTGCGG	718	
Db	1179	GTAACGCTGATCATCGCAGCCTGGGGCAGGGCCCTCGGTGAGAAAGCCCTCAAG-	1237	
Qy	719	TTTTCTACAGAAAGCACTACCAATCATCATACCTTGATCATCTTCTGTGTT	778	
Db	1238	-----ACCAAGGCAAGTGCAGATATGCCCATATAGTCTGGCAATTTCTCTGTGCT	1289	

QY 779 TCCTGCCCTATCACACTGAGACCGTCACTTG 813  
||| ||| | ||| |||  
Db 1290 TCGTCCTCCACCA CGTCAACCGCTCGCTACGTG 1332

```

RESULT 11
US-09-170-496D-181
; Sequence 181, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-coupled Receptor
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-181

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[illegible]



Qy 779 TCCTGCCCTATGACACACTGAGACCGTCCACTTG 813  
Db 743 TCGTCCCTACCACTGCAACCGCTCCGTTACGCTG 777

## RESULT 12

US-08-097-938-3  
Sequence 3, Application US/08097938  
Patent No. 5629174  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS  
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,938  
FILING DATE: 26-JUL-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHICE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22803-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..1249  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 56  
US-08-097-938-3

Query Match 8.8%; Score 92; DB 1; Length 1255;

Best Local Similarity 54.4%; Pred. No. 1.4e-18;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAACCTTCAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGGA 156  
Db 266 ACTGAAACCTGACCACTCTCTTCCATTTGTCTACAAATGTGTGTGGGGGT 325  
Qy 157 GCTTTGGGAATAGGGTTGTCCATATATGTTTCTCGACGCTTATAGAGTCCACATCT 216  
Db 326 TTGCCAAGTAAGGAGATGGCCCTGTGGGCTTTCTTTCCGAACTAAGAGAACACCT 385  
Qy 217 GTGAACGTTTTCATGCTAATCTGGGCATTTGAGATCTCTGTTATTAAGCAAGCTTCC 276  
Db 386 GCTGTGATTTTACATGCGCAATCTGGCTTGGCTGACCTCTCTGTCACTGGGTCC 445  
Qy 277 TTCAAGGCTGACTATATCTTATAGAGCTCAATTGGATATTTGAGACCTGGCTGACAG 336  
Db 446 TTGAAGATGCTCTATCACTACATCATGCAACAACTGGATTTATGGGGAAGCTTTGTAT 505

Qy 337 ATTATGCTTATTCCTGTGATGTACATAGTACAGAGATTTATTTCTGACCGGCTG 396  
Db 506 GTGCTTATTTGGCTTTTCTTATGGAACATGATCTTTCATGATGACCTGCTC 565  
Qy 397 AGCTTTGGCGTTTCTTCGCAATGGTTCAACCCCTTTGGC 436  
Db 566 AGTGTGACAGGATTTGGGTGATCGTAACCCCACTGGGAC 605

## RESULT 13

US-08-476-000-3  
Sequence 3, Application US/08476000  
Patent No. 5716789  
GENERAL INFORMATION:  
APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,000  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..1249  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 56  
US-08-476-000-3

Query Match 8.8%; Score 92; DB 1; Length 1255;

Best Local Similarity 54.4%; Pred. No. 1.4e-18;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAACCTTCAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGGA 156  
Db 266 ACTGAAACCTGACCACTCTCTTCCATTTGTCTACAAATGTGTGTGGGGGT 325  
Qy 157 GCTTTGGGAATAGGGTTGTCCATATATGTTTCTCGACGCTTATAGAGTCCACATCT 216  
Db 326 TTGCCAAGTAAGGAGATGGCCCTGTGGGCTTTCTTTCCGAACTAAGAGAACACCT 385  
Qy 217 GTGAACGTTTTCATGCTAATCTGGGCATTTGAGATCTCTGTTATTAAGCAAGCTTCC 276

Db 386 GCTGATTTACATGAGCAATCTGGCCCTTGAGCTACCTCTCTGTGCATCTGTTCC 445  
Qy 277 TTGAGGCTACTATTTATCTTAGAGCTCCAAATTGATTTATGGAGCTGGCCTGCAGG 336  
Db 446 TTGAAGATTGCTATTCATACATACATGCAACACCTGATTTATGGGAGCTCTTGTAAAT 505  
Qy 337 ATTATGCTTATTCCTTGATGTCAACATGTAGACAGATTTATTTCTGACCGTGTG 396  
Db 506 GTGCTTATTTGGCTTTTCTTATGGCAACATGATCTGTTCCATTTCTTCATGACCTGCTC 565  
Qy 397 AGTGTGTGCGTTTCTTGCAATGTTCACTCCCTTTGGC 436  
Db 566 AGTGTGACAGATTTGGTTCATGTCGTAACCCCATGGGCG 605

RESULT 14  
US-08-472-840-3  
Sequence 3, Application US/08472840  
Patent No. 5763575

## GENERAL INFORMATION:

APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,840  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..1249

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 56

US-08-472-840-3

Query Match 8.8%; Score 92; DB 1; Length 1255;  
Best Local Similarity 54.4%; Pred. No. 1,4e-18;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAAACTTCAAGAGAAATTTTCCCAATTGATATCTATATATTTTCTGGGGA 156

Db 266 ACTGAAAACTGACCACTGCTTCTTCCATTGCTACACATTTGTGTGGGGT 325  
Qy 157 GTCTGGGAAATAGGCTTTGTCATATATGTTTCTGCAAGCTTAAAGATCCATCT 216  
Db 326 TTGCCAAGTAAGGCGATGCGCTTGCGTCTTCTTTCCGAATPAAGAAAGACCTT 385  
Qy 217 GTGAAGCTTTTCATGCTAAATCTGGCATTTCAGATCTTCGTTCAATAGACGCTTCC 276  
Db 386 GCTGATTTAATGAGCCATCTGCGCTTGCTGACCTCTCTGTCACTGTGGTTCCTCC 445  
Qy 277 TTGAGGCTACTATTTATCTTAGAGCTCCAAATTGATTTATGGAGACCTGGCCTGAG 336  
Db 446 TTGAAGATTGCTATTCATACATACATGCAACACCTGATTTATGGGAAAGCTTTGTAT 505  
Qy 337 ATTATGCTTATTCCTTGATGTCAACATGTACAGCATTTATTTCTGACCGTGTG 396  
Db 506 GTGCTTATTTGGCTTTTCTTATGGCAACATGATCTGTTCCATTTCTTCATGACCTGCTC 565  
Qy 397 AGTGTGTGCGTTTCTTGCAATGTTCACTCCCTTTGGC 436  
Db 566 AGTGTGACAGATTTGGTTCATGTCGTAACCCCATGGGCG 605

## RESULT 15

US-08-476-976-3  
Sequence 3, Application US/08476976  
Patent No. 5874400

## GENERAL INFORMATION:

APPLICANT: SUNDELIN, JOHAN  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,976  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/390,301  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 2803-0006.20

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..1249

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 56

US-08-476-976-3

Query Match 8.8%; Score 92; DB 1; Length 1255;  
Best Local Similarity 54.4%; Pred. No. 1,4e-18;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAAACTTCAAGAGAAATTTTCCCAATTGATATCTATATATTTTCTGGGGA 156

Query Match 8.8%; Score 92; DB 2; Length 1255;  
Best Local Similarity 54.4%; Pred. No. 1.4e-18;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 ACTGGAAAACAGACCACTGTCTTCCATTTGTCTACACAATTGTGTGTGGTGGGT 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 GCTTGGGAAATGGGTGTCCATATATGTCTTCTGACGCTTATAGAAATCCACATCT 216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 TTGCCAAGTAAAGGCATGGCCCTGTGGGTCTTCTTTCCGAACATAAGAAAGACACCT 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 GTGAAGTTTTGATGCTAATCTGGCCATTTCAGATCTCCTGTCAATAGCAAGCTTCCC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 GCTGTGATTTACATGGCCCAATCTGGCTTGGCTGACCTCTCTCTGTCACTGTGTATCCC 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 TTCAGGGCTGACTATATCTTAAGGCTCCAAATTGGATATTTGAGAACCTTGGCTGCAGG 336
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Db 446 TTGAAGATTGCTATACATACATGSCAACAACTGSAATTATGGGGAAGCTTTGTATAT 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 ATTATGCTTATTCCTTGATGTCAACATGTAAGCAGTATTTTCTTAACCGTGTG 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 506 GTGCTTATTTGCTTTTCTATGSCAACATGTAAGTCTTCCATTCTCTCATTAACCTGCTC 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 397 AGTGTGTGCGTTTCTGSCAATGTTCAACCCCTTGGGC 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 566 AGTGTGCAAGGTATTTGGGTCACTGTAAACCCCATGGGC 605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: March 20, 2005, 02:59:21  
Job time : 208.232 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:51:04 ; Search time 4055.5 Seconds  
(without alignments)  
9770.662 Million cell updates/sec

Title: US-09-826-791a-5

Perfect score: 1041

Sequence: 1 atgagagaaattatcgtc.....gaaggaacaagaactataa 1041

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hnc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	723	69.5	758	6	CD630086 56040032J
2	714	68.6	762	6	CD630084 56040024J
3	711	68.3	745	6	CD630072 56039924J
4	709.2	68.1	726	6	CD630089 56040096H
5	693	66.6	720	7	CO959137 AGENCOURT
6	680	65.3	753	6	CD630075 56039988H
7	667.2	64.1	750	6	CD630077 56039968H
8	666	64.0	673	6	CD630069 56039916H
9	655.2	62.9	729	7	CO959148 AGENCOURT
10	651	62.5	652	6	CD630079 56040008H
11	647.4	62.2	670	6	CD630087 56040016H
12	644.8	61.9	663	6	CD630081 56040016H
13	641.4	61.6	682	6	CD630067 56039908H
14	613	58.9	729	7	CF147785 AGENCOURT
15	591	55.8	633	6	CD630066 56039816R
16	588.8	55.6	621	6	CD630074 56039932J
17	550.8	52.9	1739	3	AK008997 Mus muscu
18	521	50.0	844	6	CD630082 56040016J
19	515.6	48.5	860	6	CD630070 56039916J
20	505	48.5	848	6	CD630090 56040096J
21	478.8	46.0	827	6	CD630073 56039932H
22	470.8	45.2	798	6	CD630076 56039988J
23	463	44.5	808	6	CD630088 56040088J
24	457.8	44.0	809	6	CD630068 56039908J

25	439.6	42.2	1015	6	BY754684	BY754684
26	434.6	41.7	620	6	BI961697	BI961697 MONOI 3 D
27	428	41.1	763	6	CD630078	CD630078 56039965J
28	414.4	39.8	740	6	CD630080	CD630080 56040008J
29	412	39.6	735	6	CD630085	CD630085 56040032H
30	404.6	38.9	812	6	CD630071	CD630071 56039924H
31	369.4	35.5	605	4	BI960974	BI960974 MONOI 3 D
32	369.4	35.0	656	6	CD630083	CD630083 56040024J
33	301.2	28.9	319	8	AQ001459	AQ001459 CIT-HSP-2
34	217.2	20.9	476	5	BX481095	BX481095 DKFZ686J
35	200.4	19.3	604	1	A1178926	A1178926 EST222608
36	147.2	14.1	996	9	CL092116	CL092116 ISB1-2119
37	143.2	13.8	2755	3	AK033476	AK033476 Mus muscu
38	129	12.4	474	2	BF514464	BF514464 UI-H-BW1-
39	125	12.0	833	7	CO919341	CO919341 AGENCOURT
40	123.4	11.9	842	7	CN503141	CN503141 AGENCOURT
41	123.4	11.9	870	7	CO929273	CO929273 AGENCOURT
42	121	11.6	720	7	CF147786	CF147786 AGENCOURT
43	120.4	11.6	666	8	BZ214361	BZ214361 CH230-331
44	116.8	11.2	538	7	CV030948	CV030948 10235 Pul
45	116.4	11.2	671	6	CA376521	CA376521 654906 NC

## ALIGNMENTS

RESULT 1  
CD630086  
LOCUS 56040032J1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630086  
ACCESSION CD630086  
VERSION CD630086.1 GI:40278352  
KEYWORDS EST.  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 758)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contract: Fu GK  
JOURNAL  
COMMENT Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source location/Qualifiers  
1..758  
/organism="Homo sapiens"  
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/clone\_1lb="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 69.5%; Score 723; DB 6; Length 758;  
Best Local Similarity 98.9%; Pred. No. 2.3e-199;  
Matches 749; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

1 ATGAGAGAAAAATTATATGCTTGAACCATTCCTCGTATCGAATGGAACCAAT 60  
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2 ATGAGAGAAAAATTATATGCTTGAACCATTCCTCGTATCGAATGGAACCAAT 61  
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61 GGCACTTCAGCAATAACAGCAAGCAATGCAATGGAATTTCAAGAGATTT 120  
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62 GGCACTTCAGCAATAACAGCAAGCAATGCAATGGAATTTCAAGAGATTT 121  
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121 TTCCCAATTGATATATGATATATTTTCTGGGAGTCTTGGGAATGGTTGTCATA 180  
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122 TTCCCAATTGATATATGATATATTTTCTGGGAGTCTTGGGAATGGTTGTCATA 181  
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101 TATGTTTCTCGACCTTATAGAGTCACATCTGTGAGAGTTTCAATGCAATCG 240

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Db 182 TAGTTTCTCGAGCCTTATAGAACTCCACATCTGTGAAGCTTTTTCAGTCTAAATCTG 241
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Db 242 GCCATTTCAAGATCTCTGTTCTATAGACGCTTCCCTTCAAGGCTGACTATATCTTGA 301
Qy 301 GGCTCCCAATTGGATATTTGGAGACCTGCGCTGACGAGATTAATGCTTAATTCCTGTATGTC 360
Db 302 GGCTCCCAATTGGATATTTGGAGACCTGCGCTGACGAGATTAATGCTTAATTCCTGTATGTC 361
Qy 361 AACATGTACAGCAGTATTTATTTCTGACCGCTGCTGATGTTGTGCGCTTCTGCGCAATG 420
Db 362 AACATGTACAGCAGTATTTATTTCTGACCGCTGCTGATGTTGTGCGCTTCTGCGCAATG 421
Qy 421 GTTCAACCCCTTTGGGCTTCTGCAATGTCAACAGCATCAGAGTCCCTGATCTCTGTGGG 480
Db 422 GTTCAACCCCTTTGGGCTTCTGCAATGTCAACAGCATCAGAGTCCCTGATCTCTGTGGG 481
Qy 481 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTCTGAGCAG 540
Db 482 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTCTGAGCAG 541
Qy 541 AACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAATTGCTAGCTGACAGACC 600
Db 542 AACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAATTGCTAGCTGACAGACC 601
Qy 601 ATGAACATATATTTGCC-TTGGTGTGGGCTGCTGCTGCTCCATTTTTCACATCAGCATCTG 659
Db 602 ATGAACATATATTCCTTGTGGTGTGGGCTGCTGCTGCTCCATTTTTCACATCAGCATCTG 661
Qy 660 TTATCTGCTGATCATTCGGGCTTCTGTTAAAGTGAGAGTCCCGAATCCGGGGCTGC -GG 717
Db 662 TTATCTGCTGATCATTCGGGCTTCTGTTAAAGTGAGAGTCCCGAATCCGGGGCTGC 721
Qy 718 GTTTCACAGAGGACCTGACCAACCATCATCATCA 754
Db 722 TTTCTCCAGAGGACCTGACCAACCATCATCATCA 758

RESULT 2
LOCUS CD630084 762 bp mRNA linear EST 12-JAN-2004
DEFINITION 56040024J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630084
VERSION CD630084.1 GI:40278350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 762)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..762
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

FEATURES
source

ORIGIN
Query Match 68.6%; Score 714; DB 6; Length 762;
Best Local Similarity 99.5%; Pred. No. 9,7e-197;
Matches 748; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
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Db 2 ATGAGAGAAAATTATATGCTCTTGCAACCATCATCTCCGATACGAAAATGGAACCAAT 61
Qy 61 GGCACTTTAGGAATTAACAGCAGCAAGCACTGCAATTTGAAAATTCTCAAGAGAAATT 120
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Db 122 TTCCCAATTGTATCTGATATATTTTCTGGGAGTCTTGGGAAATGGGTTGCAATA 181
Qy 181 TAGTTTCTGCAAGCTTATAGAAATTCACATCTGGAACGTTTCAATGCTTAATCTG 240
Db 182 TAGTTTCTGCAAGCTTATAGAAATTCACATCTGGAACGTTTCAATGCTTAATCTG 241
Qy 241 GCCATTTGAGATCTCTGTTCAATAAGCAGCTTCCCTCAAGGCTGACTATATCTTGA 300
Db 242 GCCATTTGAGATCTCTGTTCAATAAGCAGCTTCCCTCAAGGCTGACTATATCTTGA 301
Qy 301 GGCTCCCAATTGGATATTTGGAGACCTGCGCTGACAGATTAATGCTTAATTCCTGTATGTC 360
Db 302 GGCTCCCAATTGGATATTTGGAGACCTGCGCTGACAGATTAATGCTTAATTCCTGTATGTC 361
Qy 361 AACATGTACAGCAGTATTTATTTCTGACCGCTGCTGATGTTGTGCGCTTCTGCGCAATG 420
Db 362 AACATGTACAGCAGTATTTATTTCTGACCGCTGCTGATGTTGTGCGCTTCTGCGCAATG 421
Qy 421 GTTCAACCCCTTTGGGCTTCTGCAATGTCAACAGCATCAGAGTCCCTGATCTCTGTGGG 480
Db 422 GTTCAACCCCTTTGGGCTTCTGCAATGTCAACAGCATCAGAGTCCCTGATCTCTGTGGG 481
Qy 481 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTCTGAGCAG 540
Db 482 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTCTGAGCAG 541
Qy 541 AACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAATTGCTAGCTGACAGACC 600
Db 542 AACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAATTGCTAGCTGACAGACC 601
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Db 602 ATGAACATATATTCCTTGTGGTGTGGGCTGCTGCTGCTCCATTTTTCACATCAGCATCTG 661
Qy 660 TTATCTGCTGATCATTCGGGCTTCTGTTAAAGTGAGAGTCCCGAATCCGGGGCTGC 716
Db 662 TTATCTGCTGATCATTCGGGCTTCTGTTAAAGTGAGAGTCCCGAATCCGGGGCTGC 721
Qy 717 GTTTCACAGAGGACCTGACCAACCATCATCATCA 748
Db 722 GTTTCACAGAGGACCTGACCAACCATCATCATCA 753

RESULT 3
LOCUS CD630072 745 bp mRNA linear EST 12-JAN-2004
DEFINITION 56039924J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630072
VERSION CD630072.1 GI:40278338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
```

Tel: 6508454102  
Email: gfu@incyte.com  
Location/Qualifiers  
1..745

FEATURES  
Source  
/organism="Homo sapiens"  
/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone\_1ib="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 68.3%; Score 711; DB 6; Length 745;  
Best Local Similarity 99.7%; Pred. No. 7, 2e-196;

Matches 733; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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DB 2 ATGAGAGAAAATTATATGCTTGGCAACCATCATCTCCGTATCAGAAATGGAACCAAT 61
OY 61 GGCACCTTCAGCAATTAACAACAGAGAACTGCACAATTGAAAACCTTCAAGAGAAATTT 120
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OY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 180
DB 122 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 181
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OY 241 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTTTATCTTAA 300
DB 242 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTTTATCTTAA 301
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DB 302 GGCTCCAATTGGATATTTGGAAGCTGGGCTGAGGATTAATGCTTAATCTGTATGTC 361
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DB 362 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGGCTTCTGAGCAATG 421
OY 421 GTTCACCCCTTTCGGCTTCTGCAATGCAACAGATCAAGAGTCCCTGGAATCCTGTGG 480
DB 422 GTTCACCCCTTTCGGCTTCTGCAATGCAACAGATCAAGAGTCCCTGGAATCCTGTGG 481
OY 481 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGGAAGTGTCTGAGCAG 540
DB 482 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGGAAGTGTCTGAGCAG 541
OY 541 AACGCAAGTGCATCATATGCTTGAAGTGAATCTGTATTAATTTGTAAGTGCAGACC 600
DB 542 AACGCAAGTGCATCATATGCTTGAAGTGAATCTGTATTAATTTGTAAGTGCAGACC 601
OY 601 ATGAATTAATATGCTTGTGGTGG-TGGGCTGCTGCTGCTCAATTTTCACTACGATCTG 659
DB 602 ATGAATTAATATGCTTGTGGTGGTGGTGGCTGCTGCTCAATTTTCACTACGATCTG 661
OY 660 TTAATCGTGAATCATTCGGGTTCTGTAA-AAGTGAAGTCCCAAGATGGGGCTGCGGG 718
DB 662 TTAATCGTGAATCATTCGGGTTCTGTAA-AAGTGAAGTCCCAAGATGGGGCTGCGGG 721
OY 719 TTTCTACAGAGAGG 733
DB 722 TTTCTACAGAGAGG 736
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RESULT 4  
CD630089 726 bp mrna linear EST 12-JAN-2004  
LOCUS CD630089  
DEFINITION 56040096H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630089

VERSION CD630089.1 GI:40278355  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Fu, G. K., Wang, J. T., Yang, J., Au-Young, J., and Stuve, L. L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
Source  
Location/Qualifiers  
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FEATURES  
Source  
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/mol\_type="mrna"  
/db\_xref="taxon:9606"  
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## ORIGIN

Query Match 68.1%; Score 709.2; DB 6; Length 726;  
Best Local Similarity 99.4%; Pred. No. 2, 4e-195;

Matches 722; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 1 ATGAGAGAAAATTATATGCTTGGCAACCATCATCTCCGTATCAGAAATGGAACCAAT 60
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DB 62 GGCACCTTCAGCAATTAACAACAGAGAACTGCACAATTGAAAACCTTCAAGAGAAATTT 121
OY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 180
DB 122 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 181
OY 181 TATGTTTCTGAGGCTTATTAAGAGTCCATCTGTGAACGTTTCAATGCTAAATCTG 240
DB 182 TATGTTTCTGAGGCTTATTAAGAGTCCATCTGTGAACGTTTCAATGCTAAATCTG 241
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DB 242 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTTTATCTTAA 301
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DB 302 GGCTCCAATTGGATATTTGGAAGCTGGGCTGAGGATTAATGCTTAATCTGTATGTC 361
OY 361 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGGCTTCTGAGCAATG 420
DB 362 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGGCTTCTGAGCAATG 421
OY 421 GTTCACCCCTTTCGGCTTCTGCAATGCAACAGATCAAGAGTCCCTGGAATCCTGTGG 480
DB 422 GTTCACCCCTTTCGGCTTCTGCAATGCAACAGATCAAGAGTCCCTGGAATCCTGTGG 481
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DB 482 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGGAAGTGTCTGAGCAG 541
OY 541 AACGCAAGTGCATCATATGCTTGAAGTGAATCTGTATTAATTTGTAAGTGCAGACC 600
DB 542 AACGCAAGTGCATCATATGCTTGAAGTGAATCTGTATTAATTTGTAAGTGCAGACC 601
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DB 602 ATGAATTAATATGCTTGTGGTGGTGGCTGCTGCTCAATTTTCACTACGATCTGT 660
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Dd	661 TATCGCATATCAATTCGGGCTTGTGTTAAAGTGGAAGTCCACGAATCGGGGCTGCGGGT	720
Oy	721 TCTCAC	726
Dd	721 TCTCAC	726
RESULT 5		
LOCUS	CO959137	720 bp mRNA linear EST 17-AUG-2000
DEFINITION	AGENCOURT_30842218 NIH MGC 146 Homo sapiens CDNA clone	
ACCESSION	IMAGE:7389737 3', mRNA sequence.	
VERSION	CO959137	
KEYWORDS	CO959137.1 GI:51323719	
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL	1 (baaes 1 to 720)	
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rml0A07 Bethesda, MD 20892 Email: cgabbs@email.nih.gov Tissue Procurement: Guthrie CDNA Resource Center CDNA Library Preparation: Guthrie CDNA Resource Center CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone Distribution Information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: RB17 row: F column: 03 High quality sequence start: 20 High quality sequence stop: 632. Location/Qualifiers 1..720	

**ORIGIN**

Query Match	66.6%	Score 693;	DB 7;	Length 720;
Best Local Similarity	99.9%;	Pred. No.1.3e-150;		
Matches 704; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

QY	336	GATTATGCTCAATCCTTATATGCAACATGACAGCATTTATTTCCGACCCGGCT	359
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QY	396	GAGTGTGTCGCTTCTGGCAATGGTCAACCCCTTGGCTGCGATGTCACACGAT	455
Db	660	GAGTGTGTCGCTTCTGGCAATGGTCAACCCCTTGGCTGCGATGTCACACGAT	601
QY	456	CAGGATGCGCTGAGTCTCTGCGGATCATATGATCCTTATCGANGGCTTCTCAATAT	515

Db	600	CAGAGTGCCTGSAATCCTCTGTGGGATCATATGAAATCCATTATCATGGCTTCCCATTAAT	541
Qy	516	GCTCCTTGACATATGGCTCTTGACACAGACGGCAGTGCATCATATGCTTTAGCTGAATCT	575
Db	540	GCTCCTTGACATATGGCTCTTGACACAGACGGCAGTGCATCATATGCTTTAGCTGAATCT	481
Qy	576	CTATATAAATTCCTAAGCTGCACAGCATGAACATATATTTGCTTGGTGGGCTGCCTGCT	635
Db	480	CTATATAAATTCCTAAGCTGCACAGCATGAACATATATTTGCTTGGTGGGCTGCCTGCT	421
Qy	636	GCCATTTTTCACATCTAGCATCTGTTATCTGTCATTCATTCGGGTTCTGTTAAAGTGA	695
Db	420	GCCATTTTTCACATCTAGCATCTGTTATCTGTCATTCATTCGGGTTCTGTTAAAGTGA	361
Qy	696	GGTCCAGAAATCGGGGCTGCGGGTTCTTCACAGAAAGGACCTGACACCATATCATATCAC	755
Db	360	GGTCCAGAAATCGGGGCTGCGGGTTCTTCACAGAAAGGACCTGACACCATATCATATCAC	301
Qy	756	CTTGATCATCTTCTCTTGTGTTCCTGCCCTATCACACATGAGAACCGTCACATGAC	815
Db	300	CTTGATCATCTTCTCTTGTGTTCCTGCCCTATCACACATGAGAACCGTCACATGAC	241
Qy	816	GACATGGAATCGGGTTTATGCAAAAGACAGACTGCATATAAGCTTTGGTTATACACTGC	875
Db	240	GACATGGAATCGGGTTTATGCAAAAGACAGACTGCATATAAGCTTTGGTTATACACTGC	181
Qy	876	CTTGGCAGACCCAAATGCTGCTCTTCAATCTCTGCTATTAATCTTGGTGGGAGAAATT	935
Db	180	CTTGGCAGACCCAAATGCTGCTCTTCAATCTCTGCTATTAATCTTGGTGGGAGAAATT	121
Qy	936	TAAAGACAGATCTAAAGTTGCACTCAGAAAAGCCATCCACAGAAAGCCAAAGACAAAGTG	995
Db	120	TAAAGACAGATCTAAAGTTGCACTCAGAAAAGCCATCCACAGAAAGCCAAAGACAAAGTG	61
Qy	996	TGTTTTCCTGTAGTGTGTGTTGAGAAAGAAACAAAGATATA	1040
Db	60	TGTTTTCCTGTAGTGTGTGTTGAGAAAGAAACAAAGATATA	17

RESULT 6	CD630075	CD630075	563039989H1	FLP Homo sapiens CDNA, mRNA sequence.	EST 12-JAN-2004
LOCUS	CD630075	753 bp			
DEFINITION	CD630075	linear			
ACCESSION	CD630075				
VERSION	CD630075.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE  
1 (bases 1 to 753)  
AUTHORS  
Fu, G. K., Wang, J. T., Yang, J., Au-Yang, J., and Stuve, L. L.  
TITLE  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL  
Genomics 84 (1), 205-210 (2004)  
COMMENT  
Contact: Fu GK

FEATURES	Location/Qualifiers
source	1. .753

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ORIGIN
/Note="Vector: pDrive Cloning Vector"
Query Match      65.3%; Score 680; DB 6; Length 753;
Best Local Similarity 98.4%; Pred. No. 8.2e-187;
Matches 740; Conservative 0; Mismatches 5; Indels 7; Gaps 5;

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 QY 181 TATGTTTCTCGAGCTTATTAAGAGTCCACATCTGTAAACCTTTTCATGCTTAATCTG 240  
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 QY 421 GTTCAACCTTTGCGCTTGCATGTCAACAGATCAGAGATGCTGAAATCTCTGTGG 480  
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 Db 482 ATCATATGATCTTATCATAGCTTCTCAATTAATGCTCTGAGCAGTCTCTGAGCAG 541  
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 QY 600 CATGAACCTATATGCTTGTGGTGGCTGCTGCTGCA-TTTTTCACACTGAGATCT 658  
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 QY 718 GTTTCTC--ACAGAGAGCAGTGAACCAT 746  
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 Db 721 GGTTCTCAGCAGAGAGCAGTGAACCAT 752  
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RESULT 7  
 LOCUS CD630077 750 bp mRNA linear EST 12-JAN-2004  
 DEFINITION 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD630077  
 VERSION CD630077.1 GI:40278343  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 750)  
 Pu G.K., Wang J.T., Yang J., Au-Young J. and Strive L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 Contact: Pu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102  
 Email: gfu@incyte.com  
 Location/Qualifiers  
 FEATURES  
 source  
 1..750  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_id="FLP"  
 /note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 64.1%; Score 667.2; Db 6; Length 750;  
 Best Local Similarity 97.5%; Pred. No. 4.5e-183;  
 Matches 731; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

QY 1 ATGGAGAGAAAATTATATGCTTGGCAACATCCATCTCGTATCAGAAATGGAACCAAT 60  
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 Db 2 ATGGAGAGAAAATTATATGCTTGGCAACATCCATCTCGTATCAGAAATGGAACCAAT 61  
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 Db 62 GGCACCTTCAGCAATTAACAACAGCAGAGAACTGCACATTTGAAAACCTTCAAGAGAAATT 121  
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 QY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGCTTGGGAAATGGGTTGTCATA 180  
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 Db 122 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGCTTGGGAAATGGGTTGTCATA 181  
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 QY 599 CCATGAACCTATATGCTTGTGGTGGCTGCTGCTGCA-TTTTTCACACTGAGATCT 658  
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 Db 602 CCATGAACCTATATGCTTGTGGTGGCTGCTGCTGCA-TTTTTCACACTGAGATCT 660  
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 QY 659 GTTATCTGCTGATCATTTGGGTTCTGTTAA-AAGTGAAGTCCAGAAATGGGGCTGCGG 717  
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RESULT 8  
 LOCUS CD630069 673 bp mRNA linear EST 12-JAN-2004  
 DEFINITION 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD630069

VERSION CD630069.1 GI:40278335  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
FEATURES  
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/clone\_lib="PLP"  
/note="Vector: pDrive Cloning Vector"  
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Best Local Similarity 100.0%; Pred. No. 9, 6e-183;  
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 62 GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121  
QY 121 TTCCCAATTGATATCTGATATATTTTCTGGGAGCTCTTGGGAAATGGGTTGCCATA 180  
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QY 181 TAGTTTCTCGAGAGCTTTAAGAAAGTCCACATCTGTGAACGTTTCAATGCTAAATCTG 240  
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DB 302 GGCTCCAAATGGAAATTTGGAGAGCTGGCTGAGAGATTAATCTTATCTTGAATGTC 361  
QY 361 AACATGTAACAGATATTTATTTCTGACCGCTGAGAGTGTGCTTCTCCGCAAG 420  
DB 362 AACATGTAACAGATATTTATTTCTGACCGCTGAGAGTGTGCTTCTCCGCAAG 421  
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QY 481 ATCATATGATCTTATCATGCTTCTGATATATCTCTGAGAGTGGCTCTGAGAG 540  
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DB 602 ATGAATATATGCTTGGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

QY 661 TATCTG 666  
DB 662 TATCTG 667  
RESULT 9  
LOCUS CO959148  
DEFINITION  
ACCESSION CO959148 729 bp mRNA linear EST 17-AUG-2004  
VERSION IMAGE:7389737 5', mRNA sequence.  
KEYWORDS CO959148.1 GI:51323730  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE 1 (bases 1 to 729)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgs@nci.nih.gov  
Tissue Procurement: Guthrie cDNA Resource Center  
cDNA Library Preparation: Guthrie cDNA Resource Center  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
plate: IRB17 row: E column: 03  
High quality sequence stop: 602.  
location/Qualifiers  
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/tissue\_type="mixed"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 146"  
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:  
multiple; ORF's were PCR-amplified (from IMAGE clones or  
from commercially available cDNA libraries) and cloned by  
the Guthrie cDNA Resource Center (www.guthrie.org/cdna)  
into pCDNA3.1. For specific information on cloning sites  
(which vary by clone), please refer to the Guthrie  
website, using the Guthrie ID given in the file  
ftp://image.llnl.gov/image\_rearrayed\_plates/IRB17.presv.dat  
a. Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 62.9%; Score 655.2; DB 7; Length 729;  
Best Local Similarity 95.1%; Pred. No. 1, 4e-179;  
Matches 696; Conservative 0; Mismatches 32; Indels 4; Gaps 2;  
QY 1 ATGAGAGAAAATTATGCTCTGCAACATCTCTCCGATCAGAAATGAAACCAAT 60  
DB 2 ATGAGAGAAAATTATGCTCTGCAACATCTCTCCGATCAGAAATGAAACCAAT 61  
QY 61 GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 62 GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121  
QY 121 TTCCCAATTGATATCTGATATATTTTCTGGGAGCTTTGGGAAATGGGTTGCCATA 180  
DB 122 TTCCCAATTGATATCTGATATATTTTCTGGGAGCTTTGGGAAATGGGTTGCCATA 181  
QY 181 TAGTTTCTCGAGAGCTTTAAGAAAGTCCACATCTGTGAACGTTTCAATGCTAAATCTG 240

Db 182 TATGTTTCCCTGACGCTTATAGAAGTCACATCTGTGAAGCTTTTCATGCTAAATCG 241  
Qy 241 GGCATTTCAGATCTCTGTTCAATAGACAGCTTCCCTTACAGGCTGACATTAATATCTTAA 300  
Db 242 GGCATTTCAGATCTCTGTTCAATAGACAGCTTCCCTTACAGGCTGACATTAATATCTTAA 301  
Qy 301 GGCCTCAATTGGATATTTGAGACCTGCGCTGACAGGATTAATGCTTAATCTTGTATGTC 360  
Db 302 GGCCTCAATTGGATATTTGAGACCTGCGCTGACAGGATTAATGCTTAATCTTGTATGTC 361  
Qy 361 AACATGTACAGCAGATTAATTTATTTCTGACCGGTGAGTGTGTGGCTTCTGGCAATG 420  
Db 362 AACATGTACAGCAGATTAATTTATTTCTGACCGGTGAGTGTGTGGCTTCTGGCAATG 421  
Qy 421 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGATGCTGGATCTCTGTGGG 480  
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Qy 481 ATCATATGGATCTTATCATAGGCTTCTCATATATGCTCTGGAACAGTCTGTGAGAG 540  
Db 482 ATCATATGGATCTTATCATAGGCTTCTCATATATGCTCTGGAACAGTCTGTGAGAG 541  
Qy 541 AACGGCAGTGCATCATATGCTTAAGCTGAACTCTATATAATTGCTAAAGCTGACAGAC 600  
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Db 661 TATCTGCTGATCATTCGGGTTCTGTTAAAGTGAAGTCCAGAAATCGGGAGCTGGGGGT 717  
Qy 721 TCTCAGAGAG 732  
Db 718 TCACAAAGAAAG 729

RESULT 10  
CD630079 652 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040008H1 FLB Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630079  
ACCESSION CD630079  
VERSION CD630079.1 GI:40278345  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 652)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
LOCATION/Qualifiers  
1. 652  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLB"  
/note="Vector: pDrive Cloning Vector"  
ORIGIN  
Query Match 62.5%; Score 651; DB 6; Length 652;  
Best Local Similarity 100.0%; Pred. No. 2,3e-178;  
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGAAATTTATGTCCTTGAACCATCCATCTCGTATCAGAAATGGAACCAAT 60  
Db 2 ATGAGAGAAATTTATGTCCTTGAACCATCCATCTCGTATCAGAAATGGAACCAAT 61  
Qy 61 GGCACCTTCAGCAATPAACAACAGAGAACTGACAAATTGAAAACCTCAAGAGAGATT 120  
Db 62 GGCACCTTCAGCAATPAACAACAGAGAACTGACAAATTGAAAACCTCAAGAGAGATT 121  
Qy 121 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCTA 180  
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Qy 181 TATGTTTCCCTGACGCTTATAGAAGTCACATCTGTGAAGCTTTTCATGCTAAATCG 240  
Db 182 TATGTTTCCCTGACGCTTATAGAAGTCACATCTGTGAAGCTTTTCATGCTAAATCG 241  
Qy 241 GGCATTTCAGATCTCTGTTCAATAGACAGCTTCCCTTACAGGCTGACATTAATCTTAA 300  
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Qy 301 GGCCTCAATTGGATATTTGAGACCTGCGCTGACAGGATTAATGCTTAATCTTGTATGTC 360  
Db 302 GGCCTCAATTGGATATTTGAGACCTGCGCTGACAGGATTAATGCTTAATCTTGTATGTC 361  
Qy 361 AACATGTACAGCAGATTAATTTCTGACCGGTGAGTGTGTGGCTTCTGGCAATG 420  
Db 362 AACATGTACAGCAGATTAATTTCTGACCGGTGAGTGTGTGGCTTCTGGCAATG 421  
Qy 421 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGATGCTGGATCTCTGTGGG 480  
Db 422 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGATGCTGGATCTCTGTGGG 481  
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Qy 541 AACGGCAGTGCATCATATGCTTAAGCTGAACTCTATATAATTGCTAAAGCTGACAGAC 600  
Db 542 AACGGCAGTGCATCATATGCTTAAGCTGAACTCTATATAATTGCTAAAGCTGACAGAC 601  
Qy 601 ATGAACATATATGCTTGGTGGTGGCTGCGCTGCTGACATTTTTCACACTAGCATCTGT 660  
Db 602 ATGAACATATATGCTTGGTGGTGGCTGCGCTGCTGACATTTTTCACACTAGCATCTGT 652

RESULT 11  
CD630087 670 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040008H1 FLB Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630087  
ACCESSION CD630087  
VERSION CD630087.1 GI:40278353  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 670)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
LOCATION/Qualifiers  
1. 670  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLB"  
/note="Vector: pDrive Cloning Vector"  
ORIGIN

## ORIGIN

Query Match 62.2%; Score 647.4; DB 6; Length 670;  
 Best Local Similarity 99.7%; Pred. No. 2.6e-177;  
 Matches 659; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 QY 61 GGACCTTCAGCAATPAACAACAGAGAACTGCAATGAAAACTTCAAGAGAAATTT 120  
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RESULT 12  
 LOCUS CD630081 663 bp mRNA linear EST 12-JAN-2004  
 DEFINITION 56040016H1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD630081  
 VERSION CD630081.1 GI:40278347  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 663)  
 Fu, G.-K., Wang, J.-T., Yang, J., Au-Young, J., and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 JOURNAL CONTACT: Fu GK  
 COMMENT Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 61.9%; Score 644.8; DB 6; Length 663;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-176;  
 Matches 658; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 ATGAGAGAAAATTTATGTCCTTGAACCATCATCTCCGTATCAGAAATGGAACCAAT 60  
 DB 2 ATGAGAGAAAATTTATGTCCTTGAACCATCATCTCCGTATCAGAAATGGAACCAAT 61  
 QY 61 GGACCTTCAGCAATPAACAACAGAGAACTGCAATGAAAACTTCAAGAGAAATTT 120  
 DB 62 GGACCTTCAGCAATPAACAACAGAGAACTGCAATGAAAACTTCAAGAGAAATTT 121  
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 DB 122 TTCCCAATGTATCTGATTAATTTTCTGGGAGCTTGGGAATGGCTTGCATTA 181  
 QY 181 TATGTTTCTCGAGCCTTATTAAGAATCCACATCTGTGAACGTTTTCATGCTAAATCTG 240  
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 QY 241 GCCATTTCAGATCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACTATTAATCTTGA 300  
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 QY 301 GGCTCCAAATTTGATTTTGAAGCCTGGCTGAGATTAATGCTTATTCCTTGTATGTC 360  
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 QY 421 GTTCAACCCCTTGGCTTCTGATGTACACAGCATAGAGTCTGTGATCTCTGTGG 480  
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 QY 481 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGAGCAGTGGCTTGAAGCAG 540  
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 QY 659 GT 660  
 DB 662 GT 663

RESULT 13  
 LOCUS CD630067 682 bp mRNA linear EST 12-JAN-2004  
 DEFINITION 56039908H1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD630067  
 VERSION CD630067.1 GI:40278333  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 682)  
AUTHORS Pu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Pu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source location/Qualifiers  
1..682  
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/note="Vector: pDrive Cloning Vector"

ORIGIN  
Query Match 61.6%; Score 641.4; DB 6; Length 682;  
Best Local Similarity 97.4%; Pred. No. 1.5e-175;  
Matches 663; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

1 ATGAGAGAAAATTTATGCTCTTGCACATCCATCTCCGATCAGAAATGAAACCAAT 60  
2 ATGAGAGAAAATTTATGCTCTTGCACATCCATCTCCGATCAGAAATGAAACCAAT 61  
61 GGCACCTTCAGCAATPAACAAGCAGCACTGCAATGAAACCTTCAAGAGAAATT 120  
62 GGCACCTTCAGCAATPAACAAGCAGCACTGCAATGAAACCTTCAAGAGAAATT 121  
121 TTCCCAATTGTATCTGATTAATTTTCTGGGAGTCTTGGGAAATGGATTGTCATA 180  
122 TTCCCAATTGTATCTGATTAATTTTCTGGGAGTCTTGGGAAATGGATTGTCATA 181  
181 TATGTTTCTCGACGCTTATPAAGAAATGTCACATCTGTGAACGTTTCAATGCTGA 240  
182 TATGTTTCTCGACGCTTATPAAGAAATGTCACATCTGTGAACGTTTCAATGCTGA 241  
241 GGCATTTCAGATCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACATTAATCTTAA 300  
242 GGCATTTCAGATCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACATTAATCTTAA 301  
301 GGCCTCAATTGGAATTTTGAAGACCTGGCTGAGGATTAATCTTAAATCTTGAATGTC 360  
302 GGCCTCAATTGGAATTTTGAAGACCTGGCTGAGGATTAATCTTAAATCTTGAATGTC 361  
361 AACATGTACAGCAGATTTATTTCTGACCGTGTGAGTGTGCGTTTCTTGCGCAATG 420  
362 AACATGTACAGCAGATTTATTTCTGACCGTGTGAGTGTGCGTTTCTTGCGCAATG 421  
421 GTTCAACCCCTTTCGGCTTCTGCATGTACACAGATCAGAGTGTGCTTCTGTGGG 480  
422 GTTCAACCCCTTTCGGCTTCTGCATGTACACAGATCAGAGTGTGCTTCTGTGGG 481  
481 ATCATATGGATCTTATATCATAGGCTTCTGAATTAATGCTGGAACAGGCTCTGAGCAG 540  
482 ATCATATGGATCTTATATCATAGGCTTCTGAATTAATGCTGGAACAGGCTCTGAGCAG 541  
541 AACGCGAGTGTACATCATGCTTGAAGCTGAATCTCTATATAAA--TTGCTAAGCTGACAG 598  
542 AACGCGAGTGTACATCATGCTTGAAGCTGAATCTCTATATAAAATGCTAAGCTGACAG 601  
599 CCATGAATCTATTTGCTGT 658  
602 CCATGAATCTATTTGCTGT 661  
659 GTTATCTGCTGATCATTTGGG 679  
662 GTTATCTGCTGATCATTTGGG 682

RESULT 14  
CFL47785 729 bp mRNA linear EST 25-UTL-2003  
LOCUS AGENCOURT 14740193 NIH MGC 145 Homo sapiens cDNA clone  
DEFINITION IMAGE:6971946 5', mRNA sequence.  
ACCESSION CFL47785  
VERSION CFL47785.1 GI:33244053  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 729)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: C9apbs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRBI02 row: f column: 05  
High quality sequence stop: 659.

FEATURES  
source location/Qualifiers  
1..729  
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/mol\_type="mRNA"  
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/clone="IMAGE:6971946"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_libs="NIH MGC 145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-Xmi1/Xho1-3',  
5'-EcoRV-Xmi1/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/earrayed\_plates/IRBI.presv.dat  
a Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 58.9%; Score 613; DB 7; Length 729;  
Best Local Similarity 100.0%; Pred. No. 3e-167;  
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGAGAAAATTTATGCTCTTGCACATCCATCTCCGATCAGAAATGAAACCAAT 60  
117 ATGAGAGAAAATTTATGCTCTTGCACATCCATCTCCGATCAGAAATGAAACCAAT 176  
61 GGCACCTTCAGCAATPAACAAGCAGCACTGCAATGAAACCTTCAAGAGAAATT 120  
177 GGCACCTTCAGCAATPAACAAGCAGCACTGCAATGAAACCTTCAAGAGAAATT 236  
121 TTCCCAATTGTATCTGATTAATTTTCTGGGAGTCTTGGGAAATGGATTGTCATA 180  
237 TTCCCAATTGTATCTGATTAATTTTCTGGGAGTCTTGGGAAATGGATTGTCATA 296  
181 TATGTTTCTCGACGCTTATPAAGATCCACATCTGTGAACGTTTCAATGCTGAATCTG 240  
297 TATGTTTCTCGACGCTTATPAAGATCCACATCTGTGAACGTTTCAATGCTGAATCTG 356  
241 GGCATTTCAGATCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACATTAATCTTAA 300

Db 357 GCCATTTCAGATCTCTGTTTCATAGACAGCTTCCCTTACAGGGCTACCTATTATCTTAA 416  
Qy 301 GGCTCCAAATTTGATATTTGGAGACCTGGCTGCAGAGATTATGCTTATTCCTTGATATGTC 360  
Db 417 GGCTCCAAATTTGATATTTGGAGACCTGGCTGCAGAGATTATGCTTATTCCTTGATATGTC 476  
Qy 361 AACATGTACAGAGATATTTATTTCTGACCCGCTGAGAGTTGTGGGTTTCCGGCAATG 420  
Db 477 AACATGTACAGAGATATTTATTTCTGACCCGCTGAGAGTTGTGGGTTTCCGGCAATG 536  
Qy 421 GTTCAACCCCTTTCGGCTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 480  
Db 537 GTTCAACCCCTTTCGGCTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 596  
Qy 481 ATCATATGTATCTTATATCATGCTTCTCTCAATATATGCTCTGACAGTGGCTTGACAG 540  
Db 597 ATCATATGTATCTTATATCATGCTTCTCTCAATATATGCTCTGACAGTGGCTTGACAG 656  
Qy 541 AACGGCAGTGCATCATCATGCTTAGAGCTGAATCTCTATAAATTGCTAAGCTGCAGACC 600  
Db 657 AACGGCAGTGCATCATCATGCTTAGAGCTGAATCTCTATAAATTGCTAAGCTGCAGACC 716  
Qy 601 ATGAACCTATATTTG 613  
Db 717 ATGAACCTATATTTG 729

RESULT 15  
CD630066 633 bp mRNA linear EST 12-JAN-2004  
LOCUS CD630066  
DERIVATION 56039816R6 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630066  
VERSION CD630066.1 GI:40278332  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 633)  
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
JOURNAL extension cloning of partial genes  
COMMENT Genomics 84 (1), 205-210 (2004)  
CONTACT: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers  
1. 633  
FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN  
Query Match 56.8%; Score 591; DB 6; Length 633;  
Best Local Similarity 99.8%; Pred. No. 7.5e-161;  
Matches 602; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGGAGAGAAATTTATGTCCTTGCAACCATCATCTCCGATACAGAAATGGAACCAAT 60  
Db 2 ATGGAGAGAAATTTATGTCCTTGCAACCATCATCTCCGATACAGAAATGGAACCAAT 61  
Qy 61 GGACACCTTCAGCATATACAGACAGAGAACTGCACAAATGAAACTTCAAGAGAGAAATTT 120  
Db 62 GGACACCTTCAGCATATACAGACAGAGAACTGCACAAATGAAACTTCAAGAGAGAAATTT 121  
Qy 121 TTCCCAATTGTATATCTGATATATATTTTCTGAGGAGTCTTGGAATGGGTTGTCCATA 180  
Db 122 TTCCCAATTGTATATCTGATATATATTTTCTGAGGAGTCTTGGAATGGGTTGTCCATA 181

Qy 181 TATGTTTCTCGAGCCTTATATAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 240  
Db 182 TATGTTTCTCGAGCCTTATATAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 241  
Qy 241 GCCATTTCAGATCTCTGTTCTTAAAGACAGCTTCCCTTCAGGGCTGACTATATCTTAA 300  
Db 242 GCCATTTCAGATCTCTGTTCTTAAAGACAGCTTCCCTTCAGGGCTGACTATATCTTAA 301  
Qy 301 GGCTCCAAATTTGATATTTGGAGACCTGGCTGCAGAGTTATGCTTATTCCTTGATATGTC 360  
Db 302 GGCTCCAAATTTGATATTTGGAGACCTGGCTGCAGAGTTATGCTTATTCCTTGATATGTC 361  
Qy 361 AACATGTACAGAGATATTTATTTCTGACCCGCTGAGAGTTGTGGGTTTCCGGCAATG 420  
Db 362 AACATGTACAGAGATATTTATTTCTGACCCGCTGAGAGTTGTGGGTTTCCGGCAATG 421  
Qy 421 GTTCAACCCCTTTCGGCTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 480  
Db 422 GTTCAACCCCTTTCGGCTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 481  
Qy 481 ATCATATGTATCTTATATCATGCTTCTCTCAATATATGCTCTGAGACAGTGGCTTGACAG 540  
Db 482 ATCATATGTATCTTATATCATGCTTCTCTCAATATATGCTCTGAGACAGTGGCTTGACAG 541  
Qy 541 AACGGCAGTGCATCATCATGCTTAGAGC-TGAATCTATAAATTGCTAAGCTGCAGAC 599  
Db 542 AACGGCAGTGCATCATCATGCTTAGAGCTGAATCTCTATAAATTGCTAAGCTGCAGAC 601  
Qy 600 CAT 602  
Db 602 CAT 604

Search completed: March 20, 2005, 02:52:32  
Job time : 4057.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:56 ; Search time 30.7544 Seconds  
(without alignments)  
800.996 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712

Sequence: 1 MERNPTFSNNRNCTIENF.....KAKTKCVFVSVWLAKITRV 330

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703	99.5	346	4	US-09-585-876-2
2	559	32.7	337	3	US-09-044-404A-2
3	559	32.7	337	4	US-09-586-924-2
4	479	28.0	339	1	US-08-153-848-44
5	479	28.0	339	2	US-08-812-871-3
6	479	28.0	339	3	US-09-299-843A-44
7	479	28.0	339	3	US-09-088-337B-44
8	479	28.0	339	4	US-09-170-496D-32
9	479	28.0	339	5	PCT-US93-11153-44
10	479	28.0	339	5	PCT-US95-07180-2
11	476	27.8	339	4	US-09-170-496D-182
12	461	26.9	362	3	US-08-513-974B-374
13	446	26.1	373	4	US-09-745-842-14
14	442	25.8	373	2	US-08-559-524A-4
15	442	25.8	373	3	US-08-749-707-4
16	442	25.8	373	4	US-09-947-922-4
17	440	25.7	361	1	US-08-383-750-4
18	440	25.7	361	4	US-08-352-678-4
19	440	25.7	361	4	US-09-536-954-4
20	440	25.7	361	4	US-09-170-496D-78
21	440	25.7	361	5	PCT-US92-583B-4
22	440	25.7	361	5	PCT-US93-09636-4
23	439.5	25.7	348	3	US-08-852-824-17
24	439	25.6	302	2	US-08-467-948A-30
25	439	25.6	302	3	US-08-467-947A-30
26	437	25.5	344	2	US-08-467-948A-8
27	437	25.5	344	3	US-08-467-947A-8

28	434	25.4	361	4	US-09-170-496D-206	Sequence 206, App
29	434	25.4	377	4	US-09-745-842-17	Sequence 17, Appl
30	430	25.1	370	3	US-08-781-250-2	Sequence 2, Appl
31	424.5	24.8	374	4	US-09-745-842-15	Sequence 15, Appl
32	419.5	24.5	373	4	US-09-102-710B-3	Sequence 3, Appl
33	416.5	24.3	373	3	US-09-513-974B-373	Sequence 373, App
34	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appl
35	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appl
36	416	24.3	375	1	US-08-444-581B-2	Sequence 2, Appl
37	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appl
38	416	24.3	375	2	US-08-559-524A-3	Sequence 3, Appl
39	416	24.3	375	4	US-08-749-707-3	Sequence 3, Appl
40	416	24.3	375	3	US-09-947-922-3	Sequence 3, Appl
41	409.5	23.9	342	4	US-09-054-272-2	Sequence 2, Appl
42	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appl
43	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appl
44	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appl
45	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-09-585-876-2

Sequence 2, Application US/09585876

Patent No. 6586205

GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria Alexandra

APPLICANT: Silos-Santiago, Immaculada

TITLE OF INVENTION: 43239, A No. 6586205e1 GPCC-Like Molecule and

FILE REFERENCE: 5800-88

CURRENT APPLICATION NUMBER: US/09/585,876

CURRENT FILING DATE: 2000-06-01

EARLIER APPLICATION NUMBER: 60/182,061

EARLIER FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

US-09-585-876-2

Query Match 99.5%; Score 1703; DB 4; Length 346;

Best Local Similarity 99.4%; Pred. No. 3, 7e-124;

Matches 328; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERNPTFSNNRNCTIENFKREFPIYVLIIFPMGVNLNGLSIYFLOPKKSTSVNF	60
DB	17	MERNPTFSNNRNCTIENFKREFPIYVLIIFPMGVNLNGLSIYFLOPKKSTSVNF	76
QY	61	MNLAIISDLFFSTLPFRADYVLRGSNMFGLACRINSYSLYVMNYSIYFLTVLSVR	120
DB	77	MNLAIISDLFFSTLPFRADYVLRGSNMFGLACRINSYSLYVMNYSIYFLTVLSVR	136
QY	121	FLAMVHPRFLVHTSIRSAMIICGIIWILIMASSIMLDSGEONGSVTSCLEMLKYIA	180
DB	137	FLAMVHPRFLVHTSIRSAMIICGIIWILIMASSIMLDSGEONGSVTSCLEMLKYIA	196
QY	181	KIQTMNYIALVVGCLLPFTLSICYLLIRVLAKYEVPSGRVSRKALLTIIITLIIF	240
DB	197	KIQTMNYIALVVGCLLPFTLSICYLLIRVLAKYEVPSGRVSRKALLTIIITLIIF	256
QY	241	FLCPLPYHTLRVHTLTTWVGCKDRLHKALVITTLAANAACFNPDLTYFAGENFKDL	300
DB	257	FLCPLPYHTLRVHTLTTWVGCKDRLHKALVITTLAANAACFNPDLTYFAGENFKDL	316
QY	301	KSALRKGHPOKAKTKCVFVSVWLAKITRV	330
DB	317	KSALRKGHPOKAKTKCVFVSVWLAKITRV	346







TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-153-848-44

Query Match 28.0%; Score 479; DB 1; Length 339;  
Best Local Similarity 34.8%; Pred. No. 1.2e-29;  
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FNNNSRNTIEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPKYSTSVNVPMLNLA 65  
DB 15 FSLATAEQCGQETPEENMLFASFYLLDFLLALVGNLTALMLFIRDHKSGTPANVFLMHLA 74  
QY 66 ISDLFIISTLPFRADYLLRGSNMIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRPLAMV 125  
DB 75 VADLSCVLLPRLVLYHNSGNMHPGEIACRLTGFLFLYLMYASIFLTCISADRLAIY 134  
QY 126 HPRLLHTYSIRSAWILGIIWILI-MASSIMLDSSGQNSVTSCELENYKIACKQT 184  
DB 135 HPAVSKLKRRLPYAHILACAFMLWVAVAPLVSPOQTQNHVVCLQ--LYR-EKASH 191  
QY 165 MMYIALVGCCLRPFTLSICYLLIRVLLKVEVPESGLRVSHR--KALTITITLTIIPF 241  
DB 192 HALVSLAAVFTFPFTTTCYLLIIRSL-----RQGLRVEKRLTKAVRMIAIVAIATL 245  
QY 242 LCFPLPHTLRTVHLTTWKV--GLCKDRILKALV--ITTLAANAACFNPLVYPAGENFK 297  
DB 246 VCFVYHVNRSYVLYHYRSHGASCATQRIALANRITSCITSLNGALDPIIMYFVAEKPR 305  
QY 298 DLKSAAL---RKGNPQAKTK 315  
DB 306 HALCNILCGKRLKGPSPSEK 327

RESULT 5  
US-08-812-871-3  
Sequence 3, Application US/08812871  
Patent No. 5955303  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl  
APPLICANT: Muzong Cheng  
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,871  
FILING DATE: Filed Herewith  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0237 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 992700  
US-08-812-871-3

Query Match 28.0%; Score 479; DB 2; Length 339;  
Best Local Similarity 34.8%; Pred. No. 1.2e-29;  
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FNNNSRNTIEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPKYSTSVNVPMLNLA 65  
DB 15 FSLATAEQCGQETPEENMLFASFYLLDFLLALVGNLTALMLFIRDHKSGTPANVFLMHLA 74  
QY 66 ISDLFIISTLPFRADYLLRGSNMIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRPLAMV 125  
DB 75 VADLSCVLLPRLVLYHNSGNMHPGEIACRLTGFLFLYLMYASIFLTCISADRLAIY 134  
QY 126 HPRLLHTYSIRSAWILGIIWILI-MASSIMLDSSGQNSVTSCELENYKIACKQT 184  
DB 135 HPAVSKLKRRLPYAHILACAFMLWVAVAPLVSPOQTQNHVVCLQ--LYR-EKASH 191  
QY 165 MMYIALVGCCLRPFTLSICYLLIRVLLKVEVPESGLRVSHR--KALTITITLTIIPF 241  
DB 192 HALVSLAAVFTFPFTTTCYLLIIRSL-----RQGLRVEKRLTKAVRMIAIVAIATL 245  
QY 242 LCFPLPHTLRTVHLTTWKV--GLCKDRILKALV--ITTLAANAACFNPLVYPAGENFK 297  
DB 246 VCFVYHVNRSYVLYHYRSHGASCATQRIALANRITSCITSLNGALDPIIMYFVAEKPR 305  
QY 298 DLKSAAL---RKGNPQAKTK 315  
DB 306 HALCNILCGKRLKGPSPSEK 327

RESULT 6  
US-09-299-843A-44

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Sequence 44, Application US/09239843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bornun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Unl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-44

Query Match      28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSNRNCTIEN-FKREFFPIVYLIIFPMGVNGLSIVFLQPYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGTPANVFMLHA 74
QY 66 ISDLFIETLPFRADYYLRGSMWIFGDLACRIMSYSLVNNYSIYFLTVLSVVRFLAMV 125
DB 75 VADLSCVLPRLVYHFSGNHWPFGEIACRLTGFLFYLMNYASIFYFLTCSADRFPLAV 134
QY 126 HPRFLIHTSIRSAWILGIIWILI-MASSIMLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 135 HPAVSKLRPLVYAHLCAPLWVAVAMAPLLVSPQTVQTNHTVCLQ--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFTLSICYLLIRVLAKVEVPSGLRVSHR---KALTTIITLIIFF 241
DB 192 HALVSLAVAFTEPFTITVYCYLLIIRSL-----RQGLRVEKRLTKAVRMALVLAIFL 245
QY 242 LCFPLHYHTLRVHLTWKV--GLCKDRILKALV--ITLALAANAQENLLVYFAGENFK 297
DB 246 VCFVYHVRSVYVLYHRSHGASCATORTILALANRITSCLTSLNGALDPIWYFVAEKPR 305
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QY 298 DRUKSAL----RKGHPRKATK 315
DB 306 HALCNILCGKRLKGPSPFEGK 327

RESULT 7
US-09-088-337B-44
Sequence 44, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bornun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-JUN-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match      28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSNRNCTIEN-FKREFFPIVYLIIFPMGVNGLSIVFLQPYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGTPANVFMLHA 74
QY 66 ISDLFIETLPFRADYYLRGSMWIFGDLACRIMSYSLVNNYSIYFLTVLSVVRFLAMV 125
DB 75 VADLSCVLPRLVYHFSGNHWPFGEIACRLTGFLFYLMNYASIFYFLTCSADRFPLAV 134
QY 126 HPRFLIHTSIRSAWILGIIWILI-MASSIMLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 135 HPAVSKLRPLVYAHLCAPLWVAVAMAPLLVSPQTVQTNHTVCLQ--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFTLSICYLLIRVLAKVEVPSGLRVSHR---KALTTIITLIIFF 241
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Db 192 HALVSLAVALFPTPTVTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245  
Qy 242 LCELPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENPK 297  
Db 246 VCFVPHVNRSVYVLYHRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305  
Qy 298 DRUKSAL----RKGHPOKAKTK 315  
Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 8  
US-09-170-496D-32  
Sequence 32, Application US/09170496D  
Patent No. 6555339  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
TITLE OF INVENTION: Receptor  
FILE REFERENCE: AREN-0040  
CURRENT APPLICATION NUMBER: US/09/170,496D  
CURRENT FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-170-496D-32

Query Match 28.0%; Score 479; DB 4; Length 339;  
Best Local Similarity 34.8%; Pred. No. 1.2e-29;  
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;  
Qy 7 PSNNNSRNCITEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPYKKSSTVVNFWMLNLA 65  
Db 15 FSLATREOCQGETPEENMLFASFYLDFTLALVGNLTALMLFTRDKSGTPANVFLMHIA 74  
Qy 66 ISDLFIISTLPPRADYLLRGSNMIFGDLACRIMSYSLYVMYSSIVFLTVLSVREPLAMV 125  
Db 75 VADLSCVLLPFRLYVHBSGNHMPFGEINCRILGFLFYINMYASIVFLTCISADRLAIV 134  
Qy 126 HPRRLHVTISRSAMILCGIIVILI-MASSIMLDSGSEONGSVTSCLELNLYKAKLOT 184  
Db 135 HPVKSJLKRRLPYAHILACAFLMVVAVAMAPLLVSPQVTQTNHTVCLQ--LYR-EKASH 191  
Qy 185 MNYIALVVGCLLPFTLSICYLLIRVLKVEVPSGLRVSHR--KALTITITLIIFF 241  
Db 192 HALVSLAVALFPTPTVTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245  
Qy 242 LCELPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENPK 297  
Db 246 VCFVPHVNRSVYVLYHRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305  
Qy 298 DRUKSAL----RKGHPOKAKTK 315  
Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 9  
PCT-US93-11153-44  
Sequence 44, Application PC/TUS9311153  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schmelkarc, Vicki L.  
TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11153  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-11153-44

Query Match 28.0%; Score 479; DB 5; Length 339;  
Best Local Similarity 34.8%; Pred. No. 1.2e-29;  
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;  
Qy 7 PSNNNSRNCITEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPYKKSSTVVNFWMLNLA 65  
Db 15 FSLATREOCQGETPEENMLFASFYLDFTLALVGNLTALMLFTRDKSGTPANVFLMHIA 74  
Qy 66 ISDLFIISTLPPRADYLLRGSNMIFGDLACRIMSYSLYVMYSSIVFLTVLSVREPLAMV 125  
Db 75 VADLSCVLLPFRLYVHBSGNHMPFGEINCRILGFLFYINMYASIVFLTCISADRLAIV 134  
Qy 126 HPRRLHVTISRSAMILCGIIVILI-MASSIMLDSGSEONGSVTSCLELNLYKAKLOT 184  
Db 135 HPVKSJLKRRLPYAHILACAFLMVVAVAMAPLLVSPQVTQTNHTVCLQ--LYR-EKASH 191  
Qy 185 MNYIALVVGCLLPFTLSICYLLIRVLKVEVPSGLRVSHR--KALTITITLIIFF 241  
Db 192 HALVSLAVALFPTPTVTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245  
Qy 242 LCELPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENPK 297  
Db 246 VCFVPHVNRSVYVLYHRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305  
Qy 298 DRUKSAL----RKGHPOKAKTK 315  
Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 10  
PCT-US95-07180-2  
Sequence 2, Application PC/TUS9507180  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: GOCAYNE, JEANINE D  
APPLICANT: RUBEN, STEVEN M  
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CARBELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```
/ ADDRESS: STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/07180
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MULLINS, J.G.
/ REGISTRATION NUMBER: 30,073
/ REFERENCE/DOCKET NUMBER: 325800-366
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-07180-2
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Query Match 28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1,2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
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QY 7 FSNMNSRNCTIEN-FKREPPPIVYLIIFPWGVLGNGLSIVFLQPYKKSTSVNVFMNLTA 65
DB 15 FSLATAEQGCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGSTPANVFLMHLA 74
QY 66 ISDLFISTLPFRADYYLRGSMNWI FGDACRIMSISLYVMYSIYFLVLSVRFPLAVY 125
DB 75 VADLSCVLVPTRLVYHPSGNMPFGEIACRLTGFLFLNMYASIFFLTCISADRFLLAV 134
QY 126 HPEFLHVTISRSAMTLCGIIWILI-MASSIMLDSGSEONGSVTSCLEINLYKIATQOT 184
DB 135 HPEKSLIKRRLPYAHACFLMWVAVAMAPLIVSPQTVQTNHTVVCLO--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFFLTSLCYLLIRVLKVEVPESGLRVSHR--KALTTIIITPLIIF 241
DB 192 HALVSLAVAFPTFPITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVMTAIVLAIFL 245
QY 242 LCFPLPYHTLRVTLTWKV--GLCKDRLHKALV--ITLALAANACFNPLIYFAGEENK 297
DB 246 VCFVPHVNRSVYVLAHYRSHGASCATORILALANRITSCLTSLNGALDPIWYFVAEKFR 305
QY 298 DRKXSL---RKGHPOKAKTK 315
DB 306 HALCNILCGKRLKGPSPFEGK 327
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RESULT 11
US-09-170-496D-182
/ Sequence 182, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
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/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 182
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-170-496D-182
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Query Match 27.8%; Score 476; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 2e-29;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;
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QY 7 FSNMNSRNCTIEN-FKREPPPIVYLIIFPWGVLGNGLSIVFLQPYKKSTSVNVFMNLTA 65
DB 15 FSLATAEQGCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGSTPANVFLMHLA 74
QY 66 ISDLFISTLPFRADYYLRGSMNWI FGDACRIMSISLYVMYSIYFLVLSVRFPLAVY 125
DB 75 VADLSCVLVPTRLVYHPSGNMPFGEIACRLTGFLFLNMYASIFFLTCISADRFLLAV 134
QY 126 HPEFLHVTISRSAMTLCGIIWILI-MASSIMLDSGSEONGSVTSCLEINLYKIATQOT 184
DB 135 HPEKSLIKRRLPYAHACFLMWVAVAMAPLIVSPQTVQTNHTVVCLO--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFFLTSLCYLLIRVLKVEVPESGLRVSHR--KALTTIIITPLIIF 241
DB 192 HALVSLAVAFPTFPITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVMTAIVLAIFL 245
QY 242 LCFPLPYHTLRVTLTWKV--GLCKDRLHKALV--ITLALAANACFNPLIYFAGEENK 297
DB 246 VCFVPHVNRSVYVLAHYRSHGASCATORILALANRITSCLTSLNGALDPIWYFVAEKFR 305
QY 298 DRKXSL---RKGHPOKAKTK 315
DB 306 HALCNILCGKRLKGPSPFEGK 327
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RESULT 12
US-08-513-974B-374
/ Sequence 374, Application US/08513974B
/ Patent No. 6114139
/ GENERAL INFORMATION:
/ APPLICANT: Hinuma, Shuji
/ APPLICANT: Hosoya, Masaki
/ APPLICANT: Fujii, Ryo
/ APPLICANT: Ohtaki, Tetsuya
/ APPLICANT: Fukusumi, Shoji
/ APPLICANT: Ohgi, Kazuhito
/ TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
/ NUMBER OF SEQUENCES: 380
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/513,974B
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/JP95/01599
/ FILING DATE: 10-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 7-093989
/ FILING DATE: 19-AUG-1995
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: JP 7-057186
/ FILING DATE: 16-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 7-007177
/ FILING DATE: 20-JAN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-326611
/ FILING DATE: 28-DEC-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-270017
/ FILING DATE: 02-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-236357
/ FILING DATE: 30-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-236356
/ FILING DATE: 30-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-189274
/ FILING DATE: 11-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-189273
/ FILING DATE: 11-AUG-1945
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 6-189272
/ FILING DATE: 11-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rebnick, David S.
/ REGISTRATION NUMBER: 34, 235
/ REFERENCE/DOCKET NUMBER: 45753
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-523-3400
/ TELEFAX: 617-523-6440
/ INFORMATION FOR SEQ ID NO: 374:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 362 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-513-974B-374
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Query Match 26.9%; Score 461; DB 3; Length 362;

Best Local Similarity 30.7%; Pred. No. 3e-28; Matches 98; Conservative 81; Mismatches 114; Indels 26; Gaps 7;

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QY 5 GFPSNNRNCTI--ENFKREPPPIYVLIIFPMGVLGNGLSIYVLPQYKSTSVNFM 62
DB 21 GMAAGNATTKCSLTGTGFOFYLLPTVYIIVITGFLGNSVAIMVFHMKPMSGISVYMF 80
QY 63 NLAISDLLFISTLPFRADYYLRGSMWIFGDLACRIMSYSLYVNMYSIYFTVLSVVRFL 122
DB 81 NLALADFLVYLLPALIFYYFNKTDWIFGDVWCKLQRFIFHVNLYGSLIFLTICISVHRYT 140
QY 123 AMVHFRLLHVSISAWILGIIWILMASSIML---DSSSEONGSVTSCLE----- 173
DB 141 GVNHPLKLGRIKKNAAYVSSLVWALVVAIPLFYSGIVRNKKTIT-CYDTTADEX 199
QY 174 LNLVYKIAKIQTMVYIALVVGCLPFTLSICYLLIIRVLKVEPESGLVSHRKALTTI 233
DB 200 LRSYVYVEMCTVFMFCI-----PFIVLIGCYGLIKALIVYDLDNSPLR---RKSITYLV 251
QY 234 IITLLIIFPLCFPYHTLRTVHL-----TTWVGLCKDRIKHALVITTLAANAACFNPL 287
DB 252 IIVLTVFVAVSYLPFHVMKTMNLRLRLDFOTPQWCAFNDRVATYQVTRGIALNSCVDPI 311
QY 288 LYYPAGEFKDRLKSLARK 306
DB 312 LYFLAGDTFRRLSRATRK 330
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RESULT 13  
US-09-745-842-14

```
/ Sequence 14, Application US/09745842
/ Patent No. 6762029
/ GENERAL INFORMATION:
/ APPLICANT: Conley, Pamela B.
/ APPLICANT: Jantzen, Hans-Michael
/ APPLICANT: Ramakrishnan-Dubridge, Vanltha
/ APPLICANT: Julius, David
/ APPLICANT: Holloper, Gunter
/ APPLICANT: COR Therapeutics, Inc.
/ TITLE OF INVENTION: P2Y12 Receptor
/ FILE REFERENCE: 44481-5053-US
/ CURRENT APPLICATION NUMBER: US/09/745,842
/ CURRENT FILING DATE: 2000-12-26
/ PRIOR APPLICATION NUMBER: US 60/171,622
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 373
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
/ US-09-745-842-14
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Query Match 26.1%; Score 446; DB 4; Length 373;

Best Local Similarity 32.1%; Pred. No. 4.5e-27; Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

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QY 6 GFPSNNRNCTI--TINFKREPPPIYVLIIFPMGVLGNGLSIYVLPQYKSTSVNFM 63
DB 33 TRAVSSFKCALTKGFOFYLLPTVYIIVITGFLGNSVAIMVFHMKPMSGISVYMF 92
QY 64 LAISDLLFISTLPFRADYYLRGSMWIFGDLACRIMSYSLYVNMYSIYFTVLSVVRFL 123
DB 93 LALADFLVYLLPALIFYYFNKTDWIFGDVWCKLQRFIFHVNLYGSLIFLTICISVHRYG 152
QY 124 MWHFRLLHVSISAWILGIIWILMASSIMLDDGS--EQNGSVTSCLE-----L 174
DB 153 VYPLKSLGRLKKNAICISVLWLVVAISPILFYSGTGVKTKTIT-CYDTTSDXYL 211
QY 175 NLYKIAKIQTMVYIALVVGCLPFTLSICYLLIIRVLKVEPESGLVSHRKALTTI 234
DB 212 RSYFYSNCT---TVAMFC-VPLVLIIGCYGLIRALIKYKLDNSPLR---RKSITYLV 263
QY 235 IITLLIIFPLCFPYHTLRTVHLTT---WKVGLC--KDRIKHALVITTLAANAACFNPL 288
DB 264 IIVLTVFVAVSYLPFHVMKTMNLRLRLDFOTPQWCAFNDRVATYQVTRGIALNSCVDPI 323
QY 289 LYYPAGEFKDRLKSLARK 306
DB 324 YFLAGDTFRRLSRATRK 341
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RESULT 14  
US-08-559-524A-4

/ Sequence 4, Application US/08559524A

/ Patent No. 5871963

/ GENERAL INFORMATION:

/ APPLICANT: Conley, Pamela B.

/ APPLICANT: Jantzen, Hans-Michael

/ TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

/ NUMBER OF SEQUENCES: 14

/ CORRESPONDENCE ADDRESS:

/ ADDRESSER: MORGAN, LEWIS & BOCKIUS LLP

/ STREET: 1800 M Street, N.W.

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: USA

/ ZIP: 20036-5869

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:33 ; Search time 25.8728 Seconds  
(without alignments)  
1227.218 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712  
Sequence: 1 MEKNGTFENNNSRNCTIENF.....KAKTKCFPVSVWLAKITRV 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : 1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	467	27.3	362	2	S33733 G protein-coupled
2	447	26.1	308	2	I50241 G protein-coupled
3	446	26.1	373	2	JC4737 G protein-coupled
4	442	25.8	373	2	JC4162 P2Y receptor - bo
5	440	25.7	361	2	B45680 G protein-coupled
6	436	25.5	344	2	T09508 Intron 17 puting
7	430	25.1	370	2	JC5549 heptahelical P2Y
8	418.5	24.4	373	2	A47556 ATP receptor P2u
9	416	24.3	342	2	S13638 platelet-activati
10	416	24.3	375	2	A54946 P-2U nucleotide re
11	409.5	23.9	342	2	A40191 platelet-activatin
12	404.5	23.6	420	2	I51667 thrombin receptor
13	404	23.6	341	2	S65666 platelet activatin
14	400.5	23.4	397	2	S66518 proteinase-activat
15	398	23.2	380	2	I38435 angiotensin recept
16	397	23.2	341	2	S43252 platelet-activatin
17	394.5	23.0	355	2	A45177 chemokine (C-C) re
18	391	22.8	328	2	I55450 G protein-coupled
19	390.5	22.8	355	2	I49339 macrophage inflam
20	390	22.8	399	2	I48705 proteinase activat
21	387	22.6	371	2	JC5796 probable chemotr
22	382	22.3	371	2	JC5498 G protein-coupled
23	378.5	22.1	378	2	B55735 lymphocyte-specifi
24	378	22.1	355	2	JC5067 G protein-coupled
25	376	22.0	356	2	I49340 MIP-1 alpha recept
26	373.5	21.8	387	2	I69202 G protein-coupled
27	372.5	21.8	363	2	I57955 somatostatin recep
28	372.5	21.8	364	2	JN0763 somatostatin recep
29	372.5	21.8	378	2	A55735 G protein-coupled

30	372	21.7	363	2	I57940 somatostatin recep
31	371.5	21.7	365	2	S68208 G protein-coupled
32	370.5	21.6	383	2	S55594 G protein-coupled
33	370	21.6	365	2	S68679 G protein-coupled
34	366	21.4	355	2	G02436 chemokine (C-C) re
35	366	21.4	427	2	S17148 alpha-thrombin rec
36	364.5	21.3	362	2	JN0694 angiotensin II rec
37	363	21.2	359	2	S15403 angiotensin II rec
38	361.5	21.1	352	2	A43113 chemokine (C-C) re
39	360	21.0	432	2	A43448 thrombin receptor
40	357	20.9	328	2	JC4800 P2Y6 receptor - hu
41	356.5	20.8	333	2	I65989 G protein-coupled
42	356.5	20.8	361	2	JC5653 G protein-coupled
43	356.5	20.8	378	2	A45680 G protein-coupled
44	356	20.8	359	2	A48857 angiotensin II rec
45	356	20.8	363	2	A49092 angiotensin II rec

## ALIGNMENTS

```
RESULT 1
S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Kriebek, B.J.; Batelson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A:Reference number: S33733; MUID:93385340; PMID:8508924
A:Accession: S33733
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <MEB>
A:Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CA51716.1; PID:g395084
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      27.3% ; Score 467; DB 2; Length 362;
Best Local Similarity 30.7% ; Pred. No. 8, 7e-31;
Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps 7;

QY 5 GTFSSNNNSRNCTI--ENKRRERFPYVLIIFPWGVGLSGLSIVFLQPIYKSTSVNVFRL 62
DB 21 GWAGNATTKCSLTITGQFYFLPTVYILVFTGFLGNSVAIWMVFPHNRPMWSGISVYMF 80
QY 63 NLAISDLPISTLPFRADYLRGSMIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRFL 122
DB 81 NLALADFLVLTLPALIFYFNKKTDMIFGDVCKLQRFIFVNLVGSILFLICISVHRYT 140
QY 123 AMVHPRRLHYVTSIRSAMILGIIWILIMASSIMDL--DSGSEONGSVTSCLE----- 173
DB 141 GVVHFLKSLGRKKKNNAVVSISLVAVLAVIPLFVSQGVRRNKKITT-CYDTADDEX 199
QY 174 LNLVYIAKLQTMNYATVAVGCLLPFTTSLICVLLIRVLKVEVBSGSRVSRKALTTI 233
DB 200 LRSYFVSNCTTVPFMCI-----PVIILGCGGLIVKVLIVDLDNSPLR---RKSIVLV 251
QY 224 IITLLIFPLCPYHTLRTVHL-----TVMVGLGCKRLHKAIVTTLAANACFNPFL 287
DB 252 IIVLTVFVAVSYLFFVWMTKLNLNRLADPOTFQWCAFNDRKAVYATYQVTRKGLNSCVDP 311
QY 288 LYYPAGENFKDRLKSLARK 306
DB 312 LYFLAGDFFRRRLSRATRK 330

RESULT 2
I50241
G protein-coupled receptor 6H1 - chicken
N:Alternate names: purinoceptor 6H1
C:Species: Gallus gallus (chicken)
```

C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: I50241; J04618  
R/Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
J. Immunol. 151, 628-636, 1993  
A/Title: Identification of a G protein coupled receptor induced in activated T cells.  
A/Reference number: I50241; MUID:9332058; PMID:893036  
A/Accession: I50241  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: mRNA  
A/Residues: 1308 <KBP>  
A/Cross-references: UNIPROT:P32250; GB:I06109; NID:G304383; PIDN:AA06587.1; PID:G304386  
R/Kaplan, M.H.; Kaplan, M.G.; Barnard, E.A.  
Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
A/Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
A/Reference number: J04618; MUID:96190677; PMID:8619790  
A/Accession: J04618  
A/Molecule type: mRNA  
A/Residues: 1-308 <WEB>  
A/Cross-references: GB:I06109; NID:G304383; PIDN:AA06587.1; PID:G304384  
A/Experimental source: T-cells  
A/Comment: This receptor plays a role in T-cell activation.  
C/Genetics:  
A/Gene: P2Y5  
C/Superfamily: ATP receptor P2U  
C/Keywords: G protein-coupled receptor; transmembrane protein  
F:15-40/Domain: transmembrane #status predicted <TM1>  
F:51-74/Domain: transmembrane #status predicted <TM2>  
F:89-109/Domain: transmembrane #status predicted <TM3>  
F:133-153/Domain: transmembrane #status predicted <TM4>  
F:177-201/Domain: transmembrane #status predicted <TM5>  
F:227-248/Domain: transmembrane #status predicted <TM6>  
F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 26.1%; Score 447; DE 2; Length 308;  
Best Local Similarity 35.4%; Pred. No. 3; Db 29;  
Matches 105; Conservative 53; Mismatches 119; Indels 20; Gaps 8;

OY 12 SNNCTIE-NFKKEPPPIVLIIFPWGVLNGSLIVFLQPKKSTSVNFMNLAIISDL 70  
DB 3 SNNCTIESFKXTLLGCVFMSWFLGLNLCVAIYFTFLTKRNETTYMNLAIISDL 62  
OY 71 FISTPPFADYVLRGSNNVFGDLACRIMSYSLYVNNYSIVFLTVLSVRFPLAMHFFL 130  
DB 63 FVFLTPPLI-YFVVRNMPFGVDLCKISTVLTLYNNYGSILPLTICISVRFPAIVHPRS 121  
OY 131 LHTVSIRSAWILIGIILWILMASSI---MLDGSGBONGSVTSCLENLTKAKIQTMAY 187  
DB 122 KTLRKTRNARIVCAVWITVLASGTPASFFQSTNRQNTQGTCE-NPESPTWTKYLSR 180  
OY 188 IAL---VVGCLPEFTLSICVILLIRVLAKVEVPSGRARSHRKALTTIITLIIFELCF 244  
DB 181 IVIRIEIVGFPLILANVTCSMTVRLTKRK-PLTISRNLGSKRYLKKIIFVALVIFCFCE 239  
OY 245 LPYH-----TLRTVHLTWKVGCLKDRLEKALVITLALAAANCFNPLLYPFAGE 294  
DB 240 VPVYITLILYSIMRT---QWINGSVTVAVRMYVTLICINAVSCFPDIYVYIFSD 293

RESULT 3  
J04737  
G protein-coupled receptor P2Y1 - human  
N/Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor  
C/Species: Homo sapiens (man)  
C/Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: J04737; J04615; S54253  
R/Jensen, R.; Communi, D.; Piotrows, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.  
A/Title: Cloning and tissue distribution of the human P2Y1 receptor.  
A/Reference number: J04737; MUID:96205320; PMID:8630005  
A/Accession: J04737  
A/Molecule type: DNA  
A/Residues: 1-373 <JUN>  
A/Cross-references: UNIPROT:P47900; GB:S81950; NID:G1839438; PIDN:AA07091.1; PID:G18394

Biochem. Biophys. Res. Commun. 218:783-788, 1996

A:Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A:Reference number: J04615; MUID:96158962; PMID:8579591

A:Accession: J04615

A:Molecule type: mRNA

A:Residues: 1-373 <A>Y

A:Cross-references: GB:442029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A:Experimental source: erythro leukemia cells

R:Leon, C.; Vial, C.; Cazeneuve, J.; Gachel, C.

Submitted to the EMBL Data Library, May 1995

A:Description: Cloning of a human putative P2Y receptor.

A:Reference number: S54253

A:Accession: S54253

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137,139-373 <LEO>

A:Cross-references: EMBL:249205; NID:g798835; PIDN:CAA89066.1; PID:g798836

A:Comment: This receptor belongs to a family of G protein-coupled receptors. It responds

C:Gene: P2Y1

A:Gene: P2Y1

A:Cross-references: GDB:677125; OMIM:601167

A:Map position: 3pter-3qter

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote

F:12-77/Domain: transmembrane #status predicted <TM1>

F:12-77/Domain: transmembrane #status predicted <TM2>

F:12-77/Domain: transmembrane #status predicted <TM3>

F:124-152/Domain: transmembrane #status predicted <TM4>

F:171-191/Domain: transmembrane #status predicted <TM5>

F:214-237/Domain: transmembrane #status predicted <TM6>

F:261-282/Domain: transmembrane #status predicted <TM7>

F:305-328/Domain: transmembrane #status predicted <TM8>

F:311-37,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:358,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

F:339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depend

Query Match 26.1%; Score 446; DB 2; Length 373;

Best Local Similarity 32.1%; Pred. No. 4,6e-29;

Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY 6 TFSNNNSRNC--TIENFKKEFPPIYLLIFFMGVLGNGSIGVFLQPYKKSIVNVFMNL 63

DB 33 TAAVSSSPFCALITKGFQYIYIPAVYILVFTIGFLSNSVAIMVFVHMKPWSGISVWFN 92

QY 64 LAISDLFIETLPFRADYYLRGSNMIFGDLACRINSYSLYVMYSSIVFLTVLSVRFILA 123

DB 93 LALAPFLVYLTLPALIFYYFNKTDWIFGDAMCKLQRFIPHYVNLVYGLIFLFTCSAHRYSG 152

QY 124 MYHPRLLVHYSIRSAMLIGIIV--ILMASSIMLDGSS--EONGSVTSCLE-----L 174

DB 153 VVFPKSLIGRLKKKNAICISLVWLIVVVAISPILFYSGTGRKKTKTF--CYDPTSDEYL 211

QY 175 NLKYIAKLQTMNVYIALVVGCLLPFTLSICYLLIRVLKVEVPPSGSLVSRKALTTII 234

DB 212 RSYFIYSMT-----TVANFC--VPLVILIGCYGLIRALIVYDLNDSPLR---RKSIIYVI 263

QY 235 ITLIIIFPLCFIPYHTLRVHHITT-----WKVGLC--KDRILKALVITLALAAACENPLL 288

DB 264 IVLIVFAVSYPFVHMKTMNIRARLIDFOTPMACAFNDRVATVATYTRGLASINSQVDPIL 323

QY 289 YYPAGENFKDRLKSALRK 306

DB 324 YFLAGDTPRRRLSRATRK 341

RESULT 4

J04162

P2Y receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 12-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: J04162

C: Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.



Biochem. Biophys. Res. Commun. 212, 648-656, 1995  
A>Title: Cloning and characterization of a bovine P2Y receptor.  
A|Reference number: J04162; MUID:95352058; PMID:7626079  
A|Molecule type: mRNA  
A|Rosidues: 1-373 <HEN>  
A|Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CMA60958.1; PID:g103  
A|Experimental source: bovine endothelial cell  
C|Genetics:  
A|Gene: bomp2y  
C|Superfamily: ATP receptor P2U  
C|Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
P:52-77/Domain: transmembrane #status predicted <TM1>  
P:88-111/Domain: transmembrane #status predicted <TM2>  
P:124-150/Domain: transmembrane #status predicted <TM3>  
P:171-191/Domain: transmembrane #status predicted <TM4>  
P:214-237/Domain: transmembrane #status predicted <TM5>  
P:261-282/Domain: transmembrane #status predicted <TM6>  
P:305-328/Domain: transmembrane #status predicted <TM7>  
P:111,27,113,197/Binding site: cardonhydrate (asn) (covalent) #status predicted  
P:158/Binding site: phosphate (ser) (covalent) (by protein kinase A) #status predicted

Query Match 25.8%; Score 442; DB 2; Length 373;  
Best Local Similarity 31.0%; Pred. No. 9.8e-29;  
Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

DQ 16 TIENPREPPPIVYLIIIFWGVGLNGLSIVFLDPYKSTSVNVFMLELAISDLLFIITL 75  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 4S TKTGFQPYVLPAVYLIIVFIIGFLGNSVAIMWFVFPMKPMSSGYVMFNLADELIVLT 104  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DQ 76 PRADYYLAGSNMIFGDLACRIMSXYSLVNMYSSTIPLTVLSVAFPLAVHPEPRLLHTVS 135  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 105 PALFIFFPKNTDIFGAMCKLORFIFPVNIYGSLFTLCISAHRSYGVAYPELKSGRLK 164  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DQ 136 ISAWMLICGIIVTILIMASSIMTL---DSGEONGSVTSCL-----INLYIKLQTNN 186  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 165 KKNAYVISLVLMILVVGISPILPFGSGTGIRKKNTIT-CYDTSPSEYLRSYTIYSMT-- 221  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DQ 187 YZALVVGCLPFPTLSICYLLIIRVLKVEVPESGARVSHRKALTTITITLIFPLCFRP 246  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 222 --TVANFC-VPLVILIGCYGLVVALIYKLDNSLR---RSIYLVITVLVFNANSYTP 275  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DQ 247 VHTLRFTVHL-----TTKVGGLCKDRLHKALVTITALAANAFCNPPLYFPAGEFKRL 300  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 276 FVMMKTMNIRARLDPOPCMCAPENDRVATYQVTRGLASLNSCVDPILYFLAGDFERRRL 335  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DQ 301 KSALKR 306  
|||  
DB 336 SRATRK 341  
|||

RESULT 5  
B45680  
G protein-coupled peptide receptor EBI 2 - human  
C|Species: Homo sapiens (man)  
C|Date: 21-Sep-1993 #revision 18-Nov-1994 #text\_change 09-Jul-2004  
C|Accession: B45680  
R|Birkbach, M.; Josefsen, K.; Valamanchili, R.; Lenolt, G.; Kieff, E.  
J. Virol. 67, 2209-2220, 1993  
A|Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled P  
A|Reference number: A45680; MUID:93186173; PMID:838238  
A|Accession: B45680  
A|Status: preliminary  
A|Molecule type: nucleic acid  
A|Residues: 1-361 <BIR>  
A|Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PIDN:AAA5924.1; PID:g292057  
A|Experimental source: B-lymphocytes  
A|Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:127097)  
C|Superfamily: ATP receptor P2U  
C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match 25.7%; Score 440; DB 2; Length 361;  
Best Local Similarity 32.1%; Pred. No. 1.4e-28;

[illegible]

Db 298 IQNSIK 303

## RESULT 7

JC5549

heptahelical p2y5-like receptor - human

C:Species: Homo sapiens (man)

C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004

C:Accession: J05549

R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.

Biochem. Biophys. Res. Commun. 236, 106-112, 1997

A:Title: Cloning of a human heptahelical receptor closely related to the p2y5 receptor.

A:Reference number: J05549; MUID:97366605; PMID:9223435

A:Accession: J05549

A:Molecule type: DNA

A:Residues: 1-370 &lt;JUN&gt;

A:Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AA86322.1; PID:g2

C:Superfamily: ATP receptor P2u

Query Match 25.1%; Score 430; DB 2; Length 370;

Best Local Similarity 31.7%; Pred. No. 9.3e-28;

Matches 103; Conservative 70; Mismatches 132; Indels 20; Gaps 9;

QY 5 GTFSSNNNSRNCCTI-ENFKREFPPIVYLIIFFMGVLGNGLSIYVFLQPYKSTSVNFMIN 63

Db 23 GNATPANTT--CIYDSDFKVLNCAVYSVVFILGLITNSVSLFVFCRMRKSTALFITN 80

QY 64 LAISDLFIETLPFRADYLRGSNMIFGDLACRIMSISLYVMYSSIYFLTVLSVVRFLA 123

Db 81 LAISDLFIETLPFPKI-FYFNFRHMFEGDTLCKISGFAFLTNIGSMLFLTICISVDRLA 139

QY 124 MVAHPRLHVTISRSMILGIIIMIMASIML-LDSGEQSGSVTSCLEMLYKIAK- 181

Db 140 IVPFPSKRITRTKRNSHIVAGWMLVLSGISASLFTTNVNAATTTCEGLSKRWMTK 199

QY 182 -LQTMNYIALVVGCLLPFTLSICVLLIRVLKVEVPESGLVSHRKALTTIITLIF 240

Db 200 YLSKITFIETLVFPIILNLVSCSSVILRLK-PATLSQICOTNKKYLVKMTVMNVF 258

QY 241 FLCELFYHILRTVHLITWKVGLCK--DRLHKLIV-ITLALAAANACFNPDLIYFAGENF 296

Db 259 VVCFEYVNSVLRYALVRSQATNCFLERFPAKIMYDITLCLATLNCCEPFIYETLESF 318

QY 297 KD-----RLKSALRKGHPOKAK 313

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

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Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 319 QKSFYINAHIRMSLEFKETETPLTK 343

QY 319 QKSFYINAHIRMSLEFKETETPLTK 343

Db 5 LEFPMNSTINGTEGDELGYKCRFNEDEFKYVLLPVSIVGVCLGLCLNVAALYIFLCRLKT 64

QY 54 STSVNFMNLAIISDLFIETLPFRADYLRGSNMIFGDLACRIMSISLYVMYSSIYFL 113

Db 65 MNASTYMHILAVSDSLVYASLPLVYYAKRDHMFSTVLCVLFYETNLVYCSIFL 124

QY 114 TVLSVVRFLAMVHPRLHVTISRSMILGIIIMIMASIML-LDSGEQSGSVTSCLEMLYKIAK- 167

Db 125 TCISVHRCLGVLRPLSHLRWGRARVAAVAVVVLVLAQCAPVLVFTTSVGRTRICH 184

QY 168 VNSCLEMLYKIAKQTMNYIALVVGCL-LPFTLSICVLLIRVLKVEVPESGLVSHRKALTTIITLIF 224

Db 185 DTSAELSHFVA-----YSSVMLGLPFAVPFVILVCYVLMARLLKPAVGTGGILPR 238

QY 225 SHRKALTTIITLIFLCELPYHTLRTVHLITWKVGL-CK--DRLHKLIVITLALAAAN 281

Db 239 ARKSVRTIALVLAVALCFEPFHVTRILVYSFRSLDLSCHTIANINMAVYKTRPLASAN 298

QY 282 ACNPDLIYFAGENFKDLKSALRKGHPOKAKT 314

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

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QY 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

Db 299 SCLDPVLYFLAQO---RLVRFARDAKPTEPT 327

C1Species: Homo sapiens (man)  
C1Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1999  
C1Accession: A54946  
R1Part: C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Hurch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A1Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic  
A1Reference number: A54946; MUID:94211846; PMID:8159738  
A1Accession: A54946  
A1Status: preliminary  
A1Molecule type: mRNA; protein  
A1Residues: 1-375 <PAR>  
A1Cross-references: GB:U07225  
A1Note: parts of this sequence were confirmed by protein sequencing  
C1Genetic8:  
A1Gene: GDB:P2UR2; HP2U; P2U  
A1Cross-references: GDB:362713; OMIM:600041  
A1Map position: 11q13.5-11q14.1  
C1Superfamily: ATP receptor P2u  
C1Keywords: G protein-coupled receptor; transmembrane protein  
  
Query Match 24.3%; Score 416; DB 2; Length 375;  
Best Local Similarity 31.6%; Pred. No. 1.3e-26;  
Matches 100; Conservative 67; Mismatches 131; Indels 18; Gaps 8;  
  
QY 4 NGTFNN-SRNCCTI-ENKREFPPIVYLIIFWGLGNGSLIYFLOPYKSTSVNFM 61  
DB 13 NGTWGDELYRCRFRNEDKYVLLPVSQVVCVLGCLNAVGLYFLCRLKTNMSTYTM 72  
QY 62 LNLAIISDLFTSTLFPADYLRGSGNWIFGDLACRIMSYSLVNMYSIYFTLVSVVF 121  
DB 73 PHLAVSDALYASLPLLYVYARGDHPSTVLCVRLFTNLXCSLFLTCSVHNC 132  
QY 122 LAMVHPRLHVTYSRSANILGIIWILIMASSIMLDSGSQNGSVTSCLEMLYKIAK 181  
DB 133 LGVLRPLSLRWGRARVAVAGVAVLVLAQAPLVYFTVSARGPLCHDTSAPELPS 192  
QY 162 LQTMVYIALVGC-L-LPEFTLSICVLLIRVLTKVEPES-GLRSHKALTTIITLI 238  
DB 193 -RFLVYSSWMLGLPRAVAVILVCVLAARRLLKPAVTSQGLPRAKKSVRTIAVVA 251  
QY 239 IFPLCFPLPYHTLRVHTLTKWVGLCKDRLHKAIVTIA-----LAAANACFNPPLYVFA 293  
DB 252 VFALCFPLPHVTRTYLYSRSIDL---SCHTINALIMAKVTRIASANSCLDPVLYFLAG 308  
QY 294 ENFKDRLKSLAKRGP 309  
DB 309 Q----RLVAFARDAKP 320  
  
RESULT 11  
A40191  
platelet-activating factor receptor - human  
C1Species: Homo sapiens (man)  
C1Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 03-Jul-2004  
C1Accession: A40191; J04079; A41079; J01359; A42831; I51923  
R1Kunz, D.; Gerard, N.P.; Gerard, C.  
J. Biol. Chem. 267, 9101-9106, 1992  
A1Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur  
A1Reference number: A40191; MUID:92250505; PMID:1374385  
A1Accession: A40191  
A1Molecule type: mRNA  
A1Residues: 1-342 <KUN>  
A1Cross-references: UNIPROT:E25105; GB:M76674; NID:9456293; PIDN:AAA60002.1; PID:9456294  
R1Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.  
Biochem. Biophys. Res. Commun. 180, 105-111, 1991  
A1Title: Characterization of a human cDNA that encodes a functional receptor for platele  
A1Reference number: J04079; MUID:92028922; PMID:1656963  
A1Accession: J04079  
A1Molecule type: mRNA  
A1Residues: 1-342 <YER>  
A1Cross-references: GB:M80436; NID:9189537; PIDN:AAA60001.1; PID:9189538  
A1Experimental source: granulocyte cell line HL-60 all  
R1Nakamura, M.; Honda, Z.; Izumi, T.; Sakaraka, C.; Mutoh, H.; Minami, M.; Bito, H.; Sey

J. Biol. Chem. 266, 20400-20405, 1991  
A1Title: Molecular cloning and expression of platelet-activating factor receptor from hu  
A1Reference number: A41079; MUID:92041873; PMID:1657923  
A1Accession: A41079  
A1Status: not compared with conceptual translation  
A1Molecule type: mRNA  
A1Residues: 1-342 <NAK>  
A1Cross-references: GB:D10202; GB:D90433; NID:9219975; PIDN:BA01050.1; PID:9219976  
R1Sugimoto, T.; Tsuchimoto, H.; McGregor, C.G.A.; Mutoh, H.; Shinizu, T.; Kurachi, Y.  
Biochem. Biophys. Res. Commun. 189, 617-624, 1992  
A1Title: Molecular cloning and characterization of the platelet-activating factor recept  
A1Reference number: J01359; MUID:93112021; PMID:1281995  
A1Accession: J01359  
A1Molecule type: mRNA  
A1Residues: 1-315; N', 317-342 <SUG>  
A1Experimental source: heart  
A1Note: the authors translated the codon AAT for residue 316 as Lys  
R1Severied, C.E.; Schweickart, V.L.; Godleka, R.; Gray, P.W.  
Genomics 13, 832-834, 1992  
A1Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns  
A1Reference number: A42831; MUID:92347866; PMID:1322356  
A1Accession: A42831  
A1Molecule type: DNA  
A1Residues: 1-226; TG', 229-342 <SEY>  
A1Cross-references: GB:M88177; NID:9190697; PIDN:AAA60214.1; PID:9190698  
A1Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBI:109814)  
R1Chae, P.B.; Halonen, M.; Regan, J.W.  
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993  
A1Title: Cloning of a human platelet-activating factor receptor gene: evidence for an int  
A1Reference number: I51923; MUID:93192035; PMID:8383507  
A1Accession: I51923  
A1Status: preliminary; translated from GB/EMBL/DBJ  
A1Molecule type: DNA  
A1Residues: 1-342 <RES>  
A1Cross-references: GB:S56396; NID:9298580; PIDN:AA82755.1; PID:9298581  
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A1Gene: GDB:PTAFR  
A1Cross-references: GDB:128806; OMIM:173393  
A1Map position: 1p35-1p34.3  
C1Superfamily: ATP receptor P2u  
C1Keywords: G protein-coupled receptor; transmembrane protein  
F117-38/Domain: transmembrane #status predicted <TRI>  
F154-75/Domain: transmembrane #status predicted <TII>  
F192-113/Domain: transmembrane #status predicted <TII>  
F1134-155/Domain: transmembrane #status predicted <TIV>  
F1184-205/Domain: transmembrane #status predicted <TRV>  
F1233-253/Domain: transmembrane #status predicted <TVI>  
F1277-297/Domain: transmembrane #status predicted <VII>  
  
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Best Local Similarity 31.3%; Pred. No. 4.1e-26;  
Matches 103; Conservative 64; Mismatches 137; Indels 25; Gaps 9;  
  
QY 1 MERNTPNNNSRNCCTIENKREFPPIVYLIIFWGLGNGSLIYF--LQPYKSTSVN 58  
DB 1 MERNTP--SHMDS-----EFRTLPPIVYSIIIFVLGVANGVLAWVAPLRYCKKENEIK 53  
QY 59 VFMNLAIISDLFTSTLFPADYLRGSGNWIFGDLACRIMSYSLVNMYSIYFTLVLSV 118  
DB 54 IFMVVLTMAADMFLFTTLPLMYIYQNGWMLPKRLCNVAGCLFPINTYCSVAFGLVIRY 113  
QY 119 VFLAMVHPRLHVTYSRSANILGIIWILIM--ASSIMLDS-----GSGONGSVTSC 171  
DB 114 NRFQAVTBPDKTAQANTKRGISLSLVVAIVGAASVFLIDSTNTVPDSAGSGVTRC 173  
QY 172 LEMNIYKAKIQTMVYIALVYVGC-L-PFTLSICVLLIRVLKVPSPSGALVSHKALT 231  
DB 174 FE-HYEKSSVPLVLIHIFVPSFPLVFLIIFCNVLIIRTLMPVQOQRNAEVKRALM 232  
QY 232 TIIITLIFPLPYHTLRVHTLTKWVGLCKDRLHKA-----VITLALAAANACFNP 287  
DB 233 MWCYVLAFFICFVHHVVG-LPWLALBELGPDGDSFHQALNDAQVTLCLSTNCVLDV 291

QY 288 LYYEAGENFKDRRLKSLRKGPQKAKTKC 316  
DB 292 IYCFLLTKRFR--KHLTKRFSWSSSRKC 317

## RESULT 12

151667  
thrombin receptor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: F51667  
R:Gerstein, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; C  
Nature 366, 648-651, 1994  
A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac  
A:Reference number: F51667; MUID:94195429; PMID:8145852  
A:Accession: F51667  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-420 <GER>  
A:Cross-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g4951

Query Match 23.6%; Score 404.5; DB 2; Length 420;  
Best Local Similarity 32.4%; Pred. No. 1.3e-25;  
Matches 99; Conservative 61; Mismatches 123; Indels 23; Gaps 6;

QY 13 RNCITF-----NFKREFPIYVLIIFFWGVGLNGLSIVFLQPYKKSTSVNVFMLNLA 65  
DB 85 RNTKAEGYQLSSQWLTVPKPSLYTVFVGLNLNLAIIIFKKVKRPVAVVNLNLA 144  
QY 66 ISDLFLSTLPFRADYYLRGNSNWIPODLACRIMSGLYVNMYSIYFLTVLSVRFVFLAVY 125  
DB 145 IADVFVSULPFLXIAHLGNDMLFPGMCRITVTAFCMYCSVLLIASISVDRFLAVY 204  
QY 126 HPRRLHVTSSRSAMILCGIILWILMASSIMLDGSGEQ---NGSVTSCLEMLYKIAKL 182  
DB 205 YPMHSLSWRTMSRAVACSFIMWISIASRTPILVTQIQIRPLDITTCGHDVLDLKDLD 264  
QY 183 QTMNYALVAVGCL----PFTLSTCYLLIRVLKAVEPESGLARSHKALTTITITL 238  
DB 265 FYIYVSSR--CLLFVFPVPIITITICYIGIRLSSSSIENS---CKKTRALFLAVVLC 319  
QY 239 IFPLCLPPLHTLRTVHLTWKVGCLCKDRHLKALVITLAAANACFNPILYFAGENFKD 298  
DB 320 VFILCGFNPVLEFLTHY---LQENAEFLYFAITILACVGSVSCCLDPLIYYASQCQR 375  
QY 299 RLKXSL 304  
DB 376 YLYSL 381

## RESULT 13

S63666  
platelet activating factor receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S63666  
R:Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.  
Biochem. J. 314, 671-678, 1996  
A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz  
A:Reference number: S63666; MUID:96239129; PMID:8670084  
A:Accession: S63666  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-341 <ISH>  
A:Cross-references: UNIPROT:Q62035; EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g125  
C:Superfamily: ATP receptor P2u

Query Match 23.6%; Score 404; DB 2; Length 341;  
Best Local Similarity 30.5%; Pred. No. 1.1e-25;  
Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

QY 1 MEPNGFSSNNRNCRNTIENFKREFPIYVLIIFFWGVGLNGLSIVF--LQPYKKSTSVN 58  
DB 11 MEPNGFSSNNRNCRNTIENFKREFPIYVLIIFFWGVGLNGLSIVF--LQPYKKSTSVN 58

DB 1 MEHNSFRVDS-----EFRTYLPFIYVSVFIILGVVANGVVLVWEANLPYSKKLNEIK 53  
QY 59 VPMNLAIISDLLFISTLPFRADYYLRGNSNWIPODLACRIMSGLYVNMYSIYFLTVLSV 118  
DB 54 IFMVNLTMADLFLITLPLMIYVYNEGDMILPNFLCNVAGCLFFINTCYSAFLGVITVY 113  
QY 119 VRFLLMHPFRLLHTSIRSAWILCGIILWILMASSIMLDGSGEQ---RQNSVTSC 171  
DB 114 NRYQAVAPYKTAQATRRKRGISLSLTIWVSIVATPSFFLADSTNVLPNKDGSGNITRC 173  
QY 172 LE-LNLVYKIAQTMNYALVAVGC-LPPEFTLSICYLLIRVLKAVEPESGLARSHKRA 229  
DB 174 FEHYEYSPILVAVHFLAF---CFIVFELFLFCNVLIHITLLQPMRQKAGVKRRA 230  
QY 230 LTTITITLIFPLCLPPLHTLRTVHLTWKVGCLCKDRHLKAL----VITLAAANACNP 285  
DB 231 LMMVCVLAFLVFIICVPHVIVQ-LPWTIAELCY-QTNFQAINDAHQITLCLLSTNCVLD 288  
QY 286 PLIYFAGENFKDRRLKSLRKGPQKAKTKC 316  
DB 289 PVIYCFLLTKRFRKHL--EKFSWSSSRKC 316

## RESULT 14

S66518  
proteinase-activated receptor 2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66518; S64709; G02131  
R:Nyström, S.; Emilsson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.  
Eur. J. Biochem. 232, 84-89, 1995  
A:Title: Molecular cloning and functional expression of the gene encoding the human prote  
A:Reference number: S66518; MUID:96048032; PMID:756175  
A:Accession: S66518  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-397 <NYS>

A:Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g1006  
R:Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn,  
Biochem. J. 314, 1009-1016, 1996  
A:Title: Molecular cloning, expression and potential functions of the human proteinase-ac  
A:Reference number: S64709; MUID:96177879; PMID:8615752  
A:Accession: S64709  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137, 'A', 139-397 <BOE>  
A:Cross-references: EMBL:U34038; NID:g1041728; PIDN:AA847871.1; PID:g1041729  
R:Kahn, M.L.; Coughlin, S.R.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: H00822  
A:Accession: G02131  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 29-397 <XAH>  
A:Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540  
C:Genetics:  
A:Map position: 5q13  
A:Introns: 28/1  
C:Superfamily: ATP receptor P2u  
F:1-36/Domain: activation peptide #status predicted <AP7>  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 23.4%; Score 400.5; DB 2; Length 397;  
Best Local Similarity 30.7%; Pred. No. 2.6e-25;  
Matches 99; Conservative 69; Mismatches 121; Indels 33; Gaps 9;

QY 24 FFPYVLIIFFWGVGLNGLSIVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYL 83  
DB 77 FLPIYVTVFVGVGPSNQMALMVFLFRTKKKGPVITYMANALADLSVIFPLXIAVHI 136  
QY 84 RGSNNIFPDLDACRIMSGLYVNMYSIYFLTVLSVRFVFLAVVHPRRLHVTSSRSAMWLC 143

Db HGNMNYGELACNVLLGFFYGNMYCSILPMTCLSQRYRWYLVNPMG---HSRKAIAI 192

QY 137 G-----TWIIIMASSIML-----LDGSEONGSVTSCLEINLYKIATQTMNY-I 188

Db 144 GSIATMLLILATVITPLVYVKOTIFIPAL-----NITTHCVLPEOLVGMDFNYFL 244

QY 193 ALVWG-LLPFFLTSLCYLLIRVLLKKEVPEPSGLRVSHRKALTTIITL-IFPLCLPY 247

Db 189 SLAIGFLPEALFITSAYVLIMRLMRSSAMBNENSR-KRKAIKLITVYLVAMVYICTPS 303

QY 245 HTLRTHLTLTKYVGLCKRMLKALVITLALMAANCFNPLIYYRAGENFKDKLSAIRKG 307

Db 248 NLLLVVHYFLIK-SQGSQHVYALYVALCLSTNSCIDPFVYFVSHDFRIMAKALL-- 360

QY 304 HPOKATKCVFPVSVMLRKETR 359

Db 361 -CRSVRTVKOMQVSLTSKHSR 361



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:51:04 ; Search time 3868.5 Seconds  
(without alignments)  
9770.662 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993  
Sequence: 1 atggaaccaaatgacacct.....gaaagaacaagatataa 993

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_eef1:\*  
2: gb\_eef2:\*  
3: gb\_hic:\*  
4: gb\_eef3:\*  
5: gb\_eef4:\*  
6: gb\_eef5:\*  
7: gb\_eef6:\*  
8: gb\_g8a1:\*  
9: gb\_g8a2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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c 1	693	69.8	720	7	CO959137
2	675	68.0	758	6	CD630086
3	666	67.1	762	6	CD630084
4	663	66.8	745	6	CD630072
5	661.2	66.6	726	6	CD630089
6	662	63.6	753	6	CD630075
7	619.2	62.4	750	6	CD630077
8	618	62.2	673	6	CD630069
9	607.2	61.1	729	7	CO959148
10	603	60.7	652	6	CD630079
11	599.4	60.4	670	6	CD630087
12	596.8	60.1	663	6	CD630081
13	593.4	59.8	682	6	CD630087
14	565	56.9	729	7	CF147785
15	543	54.7	633	6	CD630066
16	540.8	54.5	621	6	CD630074
17	539.6	54.3	1739	3	AK008997
18	521	52.5	844	6	CD630082
19	515.6	51.9	860	6	CD630070
20	505	50.9	848	6	CD630090
21	478.8	48.2	827	6	CD630073
22	470.8	47.4	798	6	CD630076
23	463	46.6	808	6	CD630088
24	457.8	46.1	809	6	CD630068

25	439.6	44.3	1015	6	BY754684
c 26	428	43.1	763	6	CD630078
c 27	414.4	41.7	740	6	CD630080
c 28	412	41.5	735	6	CD630085
c 29	404.6	40.7	812	6	CD630071
30	404.4	40.7	620	4	BI961697
31	339.2	34.2	605	4	BI960974
c 32	333	33.5	656	6	CD630083
c 33	301.2	30.3	319	8	AQ001459
34	179.4	18.1	604	1	AI178926
35	169.2	17.0	476	5	BX481095
c 36	146.8	14.8	996	9	CL092116
37	143.2	14.4	2755	3	AK033476
38	125	12.6	833	7	CO919341
39	123.4	12.4	842	7	CN503141
40	123.4	12.4	870	7	CO929273
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43	116.8	11.8	538	7	CV030948
44	116.4	11.7	671	6	CA376521
45	114	11.5	1352	3	CR67452

## ALIGNMENTS

RESULT 1  
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LOCUS AGENCOURT 30842218 NIH MGC 146 Homo sapiens cDNA clone  
DEFINITION IMAGE:7389737 3', mRNA sequence.  
ACCESSION CO959137 GI:51323719  
VERSION CO959137.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS NIH (bases 1 to 720)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaabbs-remail.nih.gov  
Tissue Procurement: Guthrie cDNA Resource Center  
cDNA Library Preparation: Guthrie cDNA Resource Center  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: IRB17 row F column: 03  
High quality sequence start: 20  
High quality sequence stop: 632.  
Location/Qualifiers

## FEATURES

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:7389737"  
/feature\_type="mixed"  
/lab\_host="DH10B (T1-Phage-resistant)"  
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file

## ORIGIN

ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat  
a. Note: this is a NIH\_MGC Library."

Query Match 69.8%; Score 693; DB 7; Length 720;  
Best Local Similarity 99.9%; Pred. No. 3e-190;  
Matches 704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 288 GATTATGCTTATTCCTGATGACATGATGACAGATGATTTATTTCTGACCGTCT 347  
DB 720 GATTATGCTTATTCCTGATGACATGATGACAGATGATTTATTTCTGACCGTCT 661  
QY 348 GAGTGTGTCGTTCTGACCAATGATTCACCCCTTGGCTTCTGATGACAGCAT 407  
DB 660 GAGTGTGTCGTTCTGACCAATGATTCACCCCTTGGCTTCTGATGACAGCAT 601  
QY 408 CAGAGTGCTGATTCCTGATGACATGATGATGATTTATTTCTGACCGTCT 467  
DB 600 CAGAGTGCTGATTCCTGATGACATGATGATGATTTATTTCTGACCGTCT 541  
QY 468 GCTCTGACAGTGTCTGACAGACAGGAGTGTGATCATGCTTAAAGCTGATCT 527  
DB 540 GCTCTGACAGTGTCTGACAGACAGGAGTGTGATCATGCTTAAAGCTGATCT 481  
QY 528 CTATATAATGCTAAGCTGACAGACATGATGATTTATTTCTGACCGTCT 587  
DB 480 CTATATAATGCTAAGCTGACAGACATGATGATTTATTTCTGACCGTCT 421  
QY 588 GGCATTTTCACTGACATCTGATTCCTGATGATTCCTGATGATTCCTGATGAT 647  
DB 420 GGCATTTTCACTGACATCTGATTCCTGATGATTCCTGATGATTCCTGATGAT 361  
QY 648 GGTCCAGATGAGGAGTGTGAGTGTCTGACAGAGGAGTGTGATGATTCCTGAT 707  
DB 360 GGTCCAGATGAGGAGTGTGAGTGTCTGACAGAGGAGTGTGATGATTCCTGAT 301  
QY 708 CTATGATCTTCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 767  
DB 300 CTATGATCTTCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 241  
QY 768 GACATGAGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 827  
DB 240 GACATGAGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 181  
QY 828 CTGAGCAGAGGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 887  
DB 180 CTGAGCAGAGGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 121  
QY 888 TAAAGCAGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 947  
DB 120 TAAAGCAGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 61  
QY 948 TGTTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 992  
DB 60 TGTTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 17

RESULT 2  
CD630086 758 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040024J1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630086  
ACCESSION CD630086.1 GI:40278352  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Fu G.-K., Wang J.-T., Yang J., Au-Young J. and Senue L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)

## COMMENT

Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers

## FEATURES

source  
1..758  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_1ib="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 68.0%; Score 675; DB 6; Length 758;  
Best Local Similarity 98.9%; Pred. No. 5.4e-185;  
Matches 701; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 ATGGAACCAATGGGACCTTGAAGCAATGACAGAGGAACTGCAATGAAAACCTTC 60  
DB 50 ATGGAACCAATGGGACCTTGAAGCAATGACAGAGGAACTGCAATGAAAACCTTC 109  
QY 61 AAGAGGAATTTTCCATTTGATATGATGATGATTTTCTGGGAGTCTTGGGAAT 120  
DB 110 AAGAGGAATTTTCCATTTGATATGATGATGATTTTCTGGGAGTCTTGGGAAT 169  
QY 121 GGGTGTCCATATATGTTTCTGACAGCTTATTAAGAGTCCATCTGTGAAGTTTTC 180  
DB 170 GGGTGTCCATATATGTTTCTGACAGCTTATTAAGAGTCCATCTGTGAAGTTTTC 229  
QY 181 ATGCAAAATCTGGACATTTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 240  
DB 230 ATGCAAAATCTGGACATTTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 289  
QY 241 TATTAATCTTGAAGGCTCCAAATTTGATGATTCCTGATGATTCCTGATGATTCCTGAT 300  
DB 290 TATTAATCTTGAAGGCTCCAAATTTGATGATTCCTGATGATTCCTGATGATTCCTGAT 349  
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DB 350 TCCCTGTATGTAACATGATGATGATTTATTTCTGACAGCTGATGATGATGATGATGAT 409  
QY 361 TTCCTGCAATGATTCACCCCTTGGCTTCTGATGATTCCTGATGATTCCTGATGATTCCT 420  
DB 410 TTCCTGCAATGATTCACCCCTTGGCTTCTGATGATTCCTGATGATTCCTGATGATTCCT 469  
QY 421 ATCTCTGTGAGATGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGAT 480  
DB 470 ATCTCTGTGAGATGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGAT 529  
QY 481 GGCCTGAGCAAGAGGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 540  
DB 530 GGCCTGAGCAAGAGGAGTGTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 589  
QY 541 AAGCTGACAGCAATGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGAT 599  
DB 590 AAGCTGACAGCAATGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGAT 649  
QY 600 ACTGAGATCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 659  
DB 650 ACTGAGATCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCTGATGATTCCT 709  
QY 660 GGGGCTGC--GGGTTTCTCAAGAGGACATGACCAATCATCATCA 706  
DB 710 GGGGCTGCAGGGTTTCTCAAGAGGACATGACCAATCATCATCA 758

RESULT 3  
CD630084 762 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040024J1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630084  
ACCESSION CD630084.1 GI:40278350  
VERSION



KEYWORDS	EST.	Homo sapiens (human)
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE	1 (bases 1 to 762)	
AUTHORS	Fu G.K., Wang J.T., Yang J., Au-Young J. and Shuve L.L.	
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes	
JOURNAL	Genomics 84 (1), 205-210 (2004)	
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gtfu@incyte.com.	
FEATURES	Location/Qualifiers	
source	1..762	
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	/mol_type="RNA"	
	/db_xref="taxon:9606"	
	/clone_11b="FLP"	
	/note="Vector: pDrive Cloning Vector"	
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Query Match	67.1%;	Score 666; DB 6; Length 762;
Best Local Similarity	99.4%;	Pred. No. 2,3e-182;
Matches	700; Conservative	0; Mismatches 0; Indels 4; Gaps 3.
Oy	1	ATGGAACCAATTTGGACCTTCGACATTAACAACAGCAGAACTGCACATTGAAAACCTTC
Db	50	ATGGAAACCAATGGCACCTTCAGCATTAACACAGCAGAACTGCACATTGAAAACCTTC
Oy	61	AAGAGAAATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGAGCTCTTGGGAAT
Db	110	AAGAGAAATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGAGCTCTTGGGAAT
Oy	121	GGGTGTCTCATATATGTTTCTCTGACGCTTAAAGAGTCACACTCTGTGAAGCTTTTC
Db	170	GGGTGTCTCATATATGTTTCTCTGACGCTTAAAGAGTCACACTCTGTGAAGCTTTTC
Oy	181	ATGCAAAATCTGGGCATTTCCAGATCTCCGTTCATTAACAGCAGCTCCCTCAGGGCTGAC
Db	230	ATGCAAAATCTGGGCATTTCCAGATCTCCGTTCATTAACAGCAGCTCCCTCAGGGCTGAC
Oy	241	TATTATCTTAAGAGCTCCCAATTGATATTTGGAGACTGGCTCGAGAGTTATGCTTAT
Db	290	TATTATCTTAAGAGCTCCCAATTGATATTTGGAGACTGGCTCGAGAGTTATGCTTAT
Oy	301	TCTTTGATGCAACATGATPAACAGCAGATTTATTTCTTGACCGTCTGAGTGTGCGGT
Db	350	TCTTTGATGCAACATGATPAACAGCAGATTTATTTCTTGACCGTCTGAGTGTGCGGT
Oy	361	TTCTCGGAATGTTACCCCTTTGGGCTTCTGCATGTGCACAGATCAAGAGTCCCTGG
Db	410	TTCTCGGAATGTTACCCCTTTGGGCTTCTGCATGTGCACAGATCAAGAGTCCCTGG
Oy	421	ATCTCTGTGGGATCATATATGATCTTATCATATGAGCTTCTCAATATATGCTCTGGACAGT
Db	470	ATCTCTGTGGGATCATATATGATCTTATCATATGAGCTTCTCAATATATGCTCTGGACAGT
Oy	481	GGCTCTGAGCAAGAGCGAGTGCATCATATGCTTAAAGCTGAATCTCTTAAATTTGCT
Db	530	GGCTCTGAGCAAGAGCGAGTGCATCATATGCTTAAAGCTGAATCTCTTAAATTTGCT
Oy	541	AAGCTGACACCATGAATATATATGCTTGTGTGTGTGGCTGCC-TGCTGCAATTTTTCAAC
Db	590	AAGCTGACACCATGAATATATATGCTTGTGTGTGTGGCTGCC-TGCTGCAATTTTTCAAC
Oy	600	ACTCAGCATCTGTATCTGTGATCATTTGGGTTCTGTATA--AAAGTGAAGGT-CCGACA
Db	650	ACTCAGCATCTGTATCTGTGATCATTTGGGTTCTGTATAAGAGTGAAGGTCCCGACA
Oy	657	ATCGGGAGCTGGGGTTTCTCAAGAGAGGACCTGACCAACATCA 700

RESULT 4	CD630072	745 bp	mRNA	linear	EST 12-JAN-2004
LOCUS	CD630072				
DEFINITION	563099242U1 FLP Homo sapiens cDNA, mRNA sequence.				
ACCESSION	CD630072				
VERSION	CD630072.1	GI:40278338			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 745)				
TITLE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, D., and Stuve, L.L.				
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes				
COMMENT	Genomics 84 (1), 205-210 (2004) Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com.				
FEATURES	Location/Qualifiers				
source	1..745				
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	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone_lib="FLP"				
	/note="Vector: pDrive Cloning Vector"				
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Query Match	66.8%; Score 663; DB 6; Length 745;				
Best Local Similarity	99.7%; Pred. No. 1.7e-181;				
Matches	685; Conservative 0; Mismatches 0; Indels 2; Gaps 2;				
Db	1 ATGAGACCAATATGACACCTTCAGCAATATACACAGAGAACTGCACATTTGAAAACCTC 60				
Qy	50 ATGAGACCAATATGACACCTTCAGCAATATACACAGAGAACTGCACATTTGAAAACCTC 109				
Db	61 AAGAGAGAAATTTTCCCAATGTATATCTGATTAATTTTCTGGGGAGCTTGGGAAAT 120				
Qy	110 AAGAGAGAAATTTTCCCAATGTATATCTGATTAATTTTCTGGGGAGCTTGGGAAAT 169				
Db	121 GGGTTCGCCATATATNGTTTCCCTCCAGCCTTATAGAAAGTCACATCTGTGAAGTTTC 180				
Qy	170 GGGTTCGCCATATATNGTTTCCCTCCAGCCTTATAGAAAGTCACATCTGTGAAGTTTC 229				
Db	181 ATGCTAAATCTGGACATTTTCAGATCTCCTGTTCAATAGACGCTTCCCTTCAGGGCTGAC 240				
Qy	230 ATGCTAAATCTGGACATTTTCAGATCTCCTGTTCAATAGACGCTTCCCTTCAGGGCTGAC 289				
Db	241 TATTATCTTGAAGCTCCCAATTTGATATTTGGAGACCTGGCTCAGAGATTATGCTTAT 300				
Qy	290 TATTATCTTGAAGCTCCCAATTTGATATTTGGAGACCTGGCTCAGAGATTATGCTTAT 349				
Db	301 TCCCTGTATATGCAACATGTATACAGAGATTTATTTCTTCGACCCGTGTGATGTTGTGGCT 360				
Qy	350 TCCCTGTATATGCAACATGTATACAGAGATTTATTTCTTCGACCCGTGTGATGTTGTGGCT 409				
Db	361 TTCTCGCAATAGTATCAACCCCTTTCCGGCTTCTGCATGTACACACACATCAGAGAGCTCG 420				
Qy	410 TTCTCGCAATAGTATCAACCCCTTTCCGGCTTCTGCATGTACACACACATCAGAGAGCTCG 469				
Db	421 ATCTCTGTGGAGTCAATATGATCTTATATCAATGAGCTTCTTCAATATATGCTCTGGACAGT 480				
Qy	470 ATCTCTGTGGAGTCAATATGATCTTATATCAATGAGCTTCTTCAATATATGCTCTGGACAGT 529				
Db	481 GGCCTCTAGAGCAAGACGGCAGTGTACATCATGCTTAAAGCTGAATCTCTATAAAATTGCT 540				
Qy	530 GGCCTCTAGAGCAAGACGGCAGTGTACATCATGCTTAAAGCTGAATCTCTATAAAATTGCT 589				

QY	541	AAGCTGCAGACCATGATAAATATATTTGGCTTGAGG-TCGGCTGCGCTGCGCATTTTTCAC	593
Db	550	AAGCTGCAGACCATGATAAATATTTGGCTTGAGGCTGGGCTGCTGCGCATTTTTCAC	649
QY	600	ACTCAGCATCTGTATATCTGCTGATCATTTGGGTTCTGTAA-AGTGAGATCCAGAT	658
Db	650	ACTCAGCATCTGTATATCTGCTGATCATTTGGGTTCTGTAAACATGAGAGTCCAGAT	709
QY	659	CGGGGCTGGGGTTTCTCAGAGAGG	685
Db	710	CGGGGCTGGGGTTTCTCAGAGAGG	736
RESULT 5			
LOCUS	CD630089	726 bp	mRNA linear EST 12-JAN-2004
DEFINITION	560400936H1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630089		
VERSION	CD630089.1	GI:40278355	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacynski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 726)		
TITLE	Fu, G.K., Wang, J.T., Yang, U., Au-Young, J. and Stuve, L.L.		
JOURNAL	extension cloning of partial genes		
COMMENT	Genomics 84 (1), 205-210 (2004)		
CONTACT	Contact: Fu GK		
INCYTE	Incyte Genomics, Inc.		
PORTER	3160 Porter Dr., Palo Alto, CA 94304, USA		
TEL	Tel: 6508454102		
EMAIL	Email: gfu@incyte.com.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..726		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
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ORIGIN			
Query Match	66.6%;	Score 661.2;	DB 6;
Best Local Similarity	99.4%;	Pred. No. 5.6e-181;	
Matches	674;	Conservative	0; Mismatches 3; Indels 1; Gaps 1;
QY	1	ATGGAACCAATGGACCTTCAGCAATATACACAGCAGAACTGCACATTTGAAAATTTC	60
Db	50	ATGGAACCAATGGACCTTCAGCAATATACACAGCAGAACTGCACATTTGAAAATTTC	109
QY	61	AAGAGAGAAATTTTCCCAATGTATATGTGATATATTTTCTGGGGAGCTTGGGAAAT	120
Db	110	AAGAGAGAAATTTTCCCAATGTATATGTGATATATTTTCTGGGGAGCTTGGGAAAT	169
QY	121	GGGTTCATATATATGTTTCTCGAGCTTATAGAAGTCACATCTGMAAGTTTTC	180
Db	170	GGGTTCATATATATGTTTCTCGAGCTTATAGAAGTCACATCTGMAAGTTTTC	229
QY	181	ATGTAAATCTGGCAATTCAGATCTCTGTTCATTAAGACGCTTCCCTTAGGGCTGAC	240
Db	230	ATGTAAATCTGGCAATTCAGATCTCTGTTCATTAAGACGCTTCCCTTAGGGCTGAC	289
QY	241	TATATCTTAGAGCTCCAAATTTGATATTTTGGAGACCTGGCTGAGGATTTATGCTTAT	300
Db	290	TATATCTTAGAGCTCCAAATTTGATATTTTGGAGACCTGGCTGAGGATTTATGCTTAT	349
QY	301	TCCTTGTATGCAACATGTACAGCAGATTTATTTCTGACCGCTGAGTGTGCGT	360
Db	350	TCCTTGTATGCAACATGTACAGCAGATTTATTTCTGACCGCTGAGTGTGCGT	409
QY	361	TTCTGTGCAATGTATCACCCTTTCCGCTTCTGATGTACACAGATCAGAGTGCCTGG	420

Df		410	TTCTCGGCAATGGTTCACCCCTTTGGCTTCTGCATGTACACAGCATCAGAAGTCCCTGG	466
QY		421	ATCTCTGTGGAGATCAATATNGAATCCTTAATCAATGAGCTTCTCTCAATATATGCTCTGGACAGT	480
Df		470	ATCTCTGTGGAGATCATATNGAATCCTTAATCAATGAGCTTCTCTCAATATATGCTCTGGACAGT	529
QY		481	GAGCTGTAGAGCAAAACGGAGTGTCACATCAATGACTTAGAGCTGAATCTCTATATAATTGCT	540
Df		530	GAGCTGTAGAGCAAAACGGAGTGTCACATCAATGACTTAGAGCTGAATCTCTATATAATTGCT	589
QY		541	AAGCTGCAGAACCATTAAGATTAATGGCTTGTGTGTGGCTGCTGCTGCCATTTTTTTCACA	600
Df		590	AAGCTGCAGAACCATTAAGATTAATGGCTTGTGTGTGGCTGCTGCTGCCATTTTTTTCACA	648
QY		601	CTCAGCATCTGTATCTGCTGATCATCTTGGGCTTCTGTAAAAGTGGAGAGTCCCAGAAATCG	660
Df		649	CTCAGCATCTGTATCTGCTGATCATCTTGGGCTTCTGTAAAAGTGGAGAGTCCCAGAAATCG	708
QY		661	GAGGCTGAGGGGTTTCTCAC	678
Df		709	GAGGCTGAGGGGTTTCTCAC	726
RESULT 6				
LOCUS	CD630075	753 bp	mRNA	linear EST 12-JAN-2004
DEFINITION	56039988H1 Flp Homo sapiens cDNA, mRNA sequence.			
ACCESSION	CD630075			
VERSION	CD630075.1	GI:40278341		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 753) Fu,G.R., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.J. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004) Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com.			
JOURNAL COMMENT	Location/Qualifiers			
FEATURES	1..753			
source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="Flp" /note="Vector: pDrive Cloning Vector"			
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Query Match	63.6%; Score 632; DB 6; Length 753;			
Best Local Similarity	98.3%; Pred. No. 1.ee-172;			
Matches 692; Conservative	0; Mismatches 5; Indels 7; Gaps 5;			
QY		1	ATGGAACCAATGGCACCTTCAGCAATTAACAACAGCAGAACTGCACAAATTGAAAACTTC	60
Df		50	ATGGAACCAATGGCACCTTCAGCAATTAACAACAGCAGAACTGCACAAATTGAAAACTTC	109
QY		61	AAGAGAAATTTTCCCAATTTGTATATCTGATATATTTTCTGGGGAGCTTGGGAAAT	120
Df		110	AAGAGAAATTTTCCCAATTTGTATATCTGATATATTTTCTGGGGAGCTTGGGAAAT	169
QY		121	GAGTTGTCATATATATGTTTTCTGACAGCTTATPAAGAGTCCACATCTGTGAACGTTTTC	180
Df		170	GAGTTGTCATATATATGTTTTCTGACAGCTTATPAAGAGTCCACATCTGTGAACGTTTTC	229
QY		181	ATGCTAAATCTGGCAATTTCAAGATCTCCGTTCTCAATAGACAGCTTCCCTTCAGAGGCTGAC	240
Df		230	ATGCTAAATCTGGCAATTTCAAGATCTCCGTTCTCAATAGACAGCTTCCCTTCAGAGGCTGAC	289

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Db 290 TATTATCTTAGAGGCTCAATTGGATTTGGAGACCTGGCCGAGAGATTAATGCTTAT 349  
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QY 301 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 360  
| | | | |  
Db 350 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 409  
| | | | |  
QY 361 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 420  
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Db 410 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 469  
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QY 421 ATCCCTGTGAGATCAATATGATCTTATCATGGCTTCTCAATATATGCTCCGAGCA 480  
| | | | |  
Db 470 ATCCCTGTGAGATCAATATGATCTTATCATGGCTTCTCAATATATGCTCCGAGCA 529  
| | | | |  
QY 481 GGCTCTGAGACAGACGGCAGTGTACATCATGCTTGAAGCTGATCTTA-TAAATTGC 539  
| | | | |  
Db 530 GGCTCTGAGACAGACGGCAGTGTACATCATGCTTGAAGCTGATCTTA-TAAATTGC 589  
| | | | |  
QY 540 TAACTGACAGACATGAACTAATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 598  
| | | | |  
Db 590 TAACTGACAGACATGAACTAATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 649  
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| | | | |  
Db 650 CACTCAGCATCTGTATCTG-CTGATCATTCGGGCTTCTTAAAGTGAAGGTCACAGA 708  
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QY 658 TCGGGGCTGGGGTTCTC--ACAGAGAGCAGTACCAACAT 698  
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Db 709 TCGGGGCTGGGGTTCTCCTCACAGAGAGCAGTACCAACAT 752  
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RESULT 7  
CD630077 750 bp mRNA linear EST 12-JAN-2004  
LOCUS 56039996H1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630077  
ACCESSION CD630077.1 GI:40278343  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 750)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
CONTACT: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source  
1..750  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone\_1lb="FLP"  
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ORIGIN  
Query Match 62.4%; Score 619.2; DB 6; Length 750;  
Best Local Similarity 97.3%; Pred. No. 9, 8e-169;  
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

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Db 50 ATGGAACCAATGGACCTTACGCAATTAACAACAGCAGAACTGCAACTGAAAACTTC 109  
| | | | |  
QY 61 AAGAGAGATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGAGCTTTGGGAAT 120  
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Db 110 AAGAGAGATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGAGCTTTGGGAAT 169  
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QY 121 GGGTGTCCATATATATTTTCTGACGCTTAATGAAGTCAATCTGTGAAGCTTTTC 180  
| | | | |  
Db 170 GGGTGTCCATATATATTTTCTGACGCTTAATGAAGTCAATCTGTGAAGCTTTTC 229  
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QY 181 AAGCAATATCTGCAATTCAGATCTCTGTCATTAAGAGCTTCCCTGAGGCTGAC 240  
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Db 220 AAGCAATATCTGCAATTCAGATCTCTGTCATTAAGAGCTTCCCTGAGGCTGAC 289  
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QY 241 TATTAATCTTAGAGGCTCAATTTGATATTTGGAGACCTGGCTGAGAGATTAATGCTTAT 300  
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Db 290 TATTAATCTTAGAGGCTCAATTTGATATTTGGAGACCTGGCTGAGAGATTAATGCTTAT 349  
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Db 350 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 409  
| | | | |  
QY 361 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 420  
| | | | |  
Db 410 TCCCTGTATGTCAACATGTACAGAGATTAATTTCTGACCGTGTGATGTGCGT 469  
| | | | |  
QY 421 ATCCCTGTGAGATCAATATGATCTTATCATGGCTTCTCAATATATGCTCCGAGCA 480  
| | | | |  
Db 470 ATCCCTGTGAGATCAATATGATCTTATCATGGCTTCTCAATATATGCTCCGAGCA 529  
| | | | |  
QY 481 GGCTCTGAGACAGACGGCAGTGTACA-TGATCTTAAAGCTGAATCTTATTAATATTC 539  
| | | | |  
Db 490 GGCTCTGAGACAGACGGCAGTGTACA-TGATCTTAAAGCTGAATCTTATTAATATTC 589  
| | | | |  
QY 530 GGCTCTGAGACAGACGGCAGTGTACA-TGATCTTAAAGCTGAATCTTATTAATATTC 589  
| | | | |  
Db 540 T-AACTGACAGACATGAACTAATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 598  
| | | | |  
QY 590 TAAAGCTCAGACATGAACTAATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 648  
| | | | |  
Db 599 CACTCAGCATCTGTATCTGATCATATTCGGGCTTCTGTTAA-AAAGTGAAGTCCACAGA 657  
| | | | |  
QY 649 AACTCAGCATCTGTATCTGATCATATTCGGGCTTCTGTTAA-AAAGTGAAGTCCACAGA 708  
| | | | |  
QY 658 TCGGGGCTGGGG--TTTCTCACAGAGAGCAGTACCAACCA 697  
| | | | |  
Db 709 TCGGGGCTGGGGTTTCTCACAGAGAGCAGTACCAACCA 750  
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RESULT 8  
CD630069 673 bp mRNA linear EST 12-JAN-2004  
LOCUS 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD630069  
ACCESSION CD630069.1 GI:40278335  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 673)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
CONTACT: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

FEATURES  
source  
1..673  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_1lb="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN  
Query Match 62.4%; Score 619.2; DB 6; Length 750;  
Best Local Similarity 97.3%; Pred. No. 9, 8e-169;  
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

QY 1 ATGGAACCAATGGACCTTACGCAATTAACAACAGCAGAACTGCAACTGAAAACTTC 60  
| | | | |  
Db 50 ATGGAACCAATGGACCTTACGCAATTAACAACAGCAGAACTGCAACTGAAAACTTC 109  
| | | | |  
QY 61 AAGAGAGATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGAGCTTTGGGAAT 120  
| | | | |



Db 649 CTCAGATCCTGTGATTCGTGATCATTCGGTTCCTTAATAATGAAG---TCNGAATC 705  
Qy 661 GGGCTGGGGGTTTCTCAGAGAG 684  
Db 706 NNGCTGGGGTTTCACAAGAAAG 729

RESULT 10  
CD630079 652 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040008H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630079  
VERSION CD630079.1 GI:40278345  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Pu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
JOURNAL  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers  
1..652  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN  
Query Match 60.7%; Score 603; DB 6; Length 652;  
Best Local Similarity 100.0%; Pred. No. 4.9e-164;  
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAACCAATGGGACCTTGACATATACACAGACGAACTGCAATGAAACTTC 60  
|||||  
50 ATGAAACCAATGGGACCTTGACATATACACAGACGAACTGCAATGAAACTTC 109  
|||||  
61 AAGAGAGATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTTGGGAAT 120  
|||||  
110 AAGAGAGATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTTGGGAAT 169  
|||||  
121 GGGTGTCCATATATGTTTTCTCGACGCTTATTAAGAACTCAATCTGTGAACGTTTTC 180  
|||||  
170 GGGTGTCCATATATGTTTTCTCGACGCTTATTAAGAACTCAATCTGTGAACGTTTTC 229  
|||||  
181 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGCTGAC 240  
|||||  
220 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGCTGAC 289  
|||||  
241 TATTAATCTTGAAGGCTCCAAATTTGATATTTGAGACCTGCGTGAAGATTAATGCTTAAT 300  
|||||  
290 TATTAATCTTGAAGGCTCCAAATTTGATATTTGAGACCTGCGTGAAGATTAATGCTTAAT 349  
|||||  
301 TCTTGTATGTACATGATGACAGATATTAATTTCTGACCGTGTGATGTTGTGCGT 360  
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350 TCTTGTATGTACATGATGACAGATATTAATTTCTGACCGTGTGATGTTGTGCGT 409  
|||||  
361 TTCCTGGCAATGAGTTCACCCCTTTGGGCTTGCAGATGTCACAGACATCAGAGTGGCTGG 420  
|||||  
410 TTCCTGGCAATGAGTTCACCCCTTTGGGCTTGCAGATGTCACAGACATCAGAGTGGCTGG 469  
|||||  
421 ATCTCTGTGGATCATATGATCTTATCATGGCTTCTCTCAATATATGCTCTCTGACAGT 480  
|||||  
470 ATCTCTGTGGATCATATGATCTTATCATGGCTTCTCTCAATATATGCTCTCTGACAGT 529  
|||||

Qy 481 GGGCTGAGACAGAGGAGGTGACATCATGCTTAGAGCTGATCTTATTAATAATGCT 540  
|||||  
Db 530 GGCTTGGACAGACGGAGGTTCATCATATGCTTAGAGCTGATCTTATTAATAATGCT 589  
|||||  
Qy 541 AAGCTGACAGACCATGAACTATATTCCTTGTGTGTGTGGGCTGCTGCAATTTTTCACA 600  
|||||  
Db 590 AAGCTGACAGACCATGAACTATATTCCTTGTGTGTGTGGGCTGCTGCAATTTTTCACA 649  
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Qy 601 CTC 603  
|||  
Db 650 CTC 652

RESULT 11  
CD630087 670 bp mRNA linear EST 12-JAN-2004  
LOCUS 56040008H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630087  
VERSION CD630087.1 GI:40278353  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Pu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
JOURNAL  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers  
1..670  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN  
Query Match 60.4%; Score 599.4; DB 6; Length 670;  
Best Local Similarity 99.7%; Pred. No. 5.5e-163;  
Matches 611; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 ATGAACCAATGGGACCTTGACATATACACAGACGAACTGCAATGAAACTTC 60  
|||||  
50 ATGAACCAATGGGACCTTGACATATACACAGACGAACTGCAATGAAACTTC 109  
|||||  
61 AAGAGAGATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTTGGGAAT 120  
|||||  
110 AAGAGAGATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTTGGGAAT 169  
|||||  
121 GGGTGTCCATATATGTTTTCTCGACGCTTATTAAGAACTCAATCTGTGAACGTTTTC 180  
|||||  
170 GGGTGTCCATATATGTTTTCTCGACGCTTATTAAGAACTCAATCTGTGAACGTTTTC 229  
|||||  
181 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGCTGAC 240  
|||||  
220 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGCTGAC 289  
|||||  
241 TATTAATCTTGAAGGCTCCAAATTTGATATTTGAGACCTGCGTGAAGATTAATGCTTAAT 300  
|||||  
290 TATTAATCTTGAAGGCTCCAAATTTGATATTTGAGACCTGCGTGAAGATTAATGCTTAAT 349  
|||||  
301 TCTTGTATGTACATGATGACAGATATTAATTTCTGACCGTGTGATGTTGTGCGT 360  
|||||  
350 TCTTGTATGTACATGATGACAGATATTAATTTCTGACCGTGTGATGTTGTGCGT 409  
|||||  
361 TTCCTGGCAATGAGTTCACCCCTTTGGGCTTGCAGATGTCACAGACATCAGAGTGGCTGG 420  
|||||

Db 410 TTCCTGCAATAGTTACCCCTTTGGCTTCTGATGTCACAGCATCAGAGTGCCTGG 469  
Qy 421 ATCTCTGTGGATCATATGATCTTATCATGCTTCTCATAATAGTCTCTGGACAGT 480  
Db 470 ATCTCTGTGGATCATATGATCTTATCATGCTTCTCATAATAGTCTCTGGACAGT 529  
Qy 481 GGCTCTGAGCAACGCGAGTGTACATCATGCTTAGAGCTGAATCTTAATAATGGT 540  
Db 530 GGCTCTGAGCAACGCGAGTGTACATCATGCTTAGAGCTGAATCTTATAAATGGT 589  
Qy 541 AAGCTGAGACCATGAATCTATTTGCTGTGGTGGGCTGCTGCTCCATTTTTCACA 600  
Db 590 AAGCTGAGACCATGAATCTATTTGCTGTGGTGGGCTG-CTGCTGCATTTTTCACA 648  
Qy 601 CTGAGCATCTGT 613  
Db 649 CTGAGCATCTGT 661

RESULT 12  
LOCUS CD630081 663 bp mRNA linear EST 12-JAN-2004  
DEFINITION 56040016H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630081  
VERSION CD630081.1 GI:40278347  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Bukayocla; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com

FEATURES  
source 1..663  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 60.1%; Score 596.8; DB 6; Length 663;  
Best Local Similarity 99.3%; Pred. No. 3.2e-162;  
Matches 610; Conservative 0; Mismatches 2; Indels 2; Gaps 1;  
Qy 1 ATGGAACCAATGCGACCTTCAGCAATTAACAAGCAGAACTGCACAATTGAAAATCTTC 60  
Db 50 ATGGAACCAATGCGACCTTCAGCAATTAACAAGCAGAACTGCACAATTGAAAATCTTC 109  
Qy 61 AAGAGAGAAATTTTCCCAATGATATCGATTAATTTTTCGGGAGTCTTGGGAAT 120  
Db 110 AAGAGAGAAATTTTCCCAATGATATCGATTAATTTTTCGGGAGTCTTGGGAAT 169  
Qy 121 GGGTTGTCATATATGTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 180  
Db 170 GGGTTGTCATATATGTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 229  
Qy 181 AAGCTAAATCTGGCCATTCAGATCTCTGTTCAATAGACGCTTCCCTTCAAGGCTGAC 240  
Db 230 AAGCTAAATCTGGCCATTCAGATCTCTGTTCAATAGACGCTTCCCTTCAAGGCTGAC 289  
Qy 241 TATTAATCTTGAAGGCTCCAAATGATATTTGAGACCTGGCTGAGAGATTAATGCTTAT 300  
Db 290 TATTAATCTTGAAGGCTCCAAATGATATTTGAGACCTGGCTGAGAGATTAATGCTTAT 349

Qy 301 TCTTGTATGCAACATGTAAGCAATATTTATTTCTGACCCGTGTAGTGTGTGCGT 360  
Db 350 TCTTGTATGCAACATGTAAGCAATATTTATTTCTGACCCGTGTAGTGTGTGCGT 409  
Qy 361 TTCCTGGCAATGATTAACCCCTTTGGCTTTCGCAATGTCACAGATCAGAGTGCCTGG 420  
Db 410 TTCCTGGCAATGATTAACCCCTTTGGCTTTCGCAATGTCACAGATCAGAGTGCCTGG 469  
Qy 421 ATCTCTGTGGATCATATGATCTTATCATGCTTCTCATAATAGTCTCTGGACAGT 480  
Db 470 ATCTCTGTGGATCATATGATCTTATCATGCTTCTCATAATAGTCTCTGGACAGT 529  
Qy 481 GGCTCTGAGCAACGCGAGTGTACATCATGCTTAGAGCTGAATCTTAATAATGGT 540  
Db 530 GGCTCTGAGCAACGCGAGTGTACATCATGCTTAGAGCTGAATCTTATAAATGGT 589  
Qy 541 AAGCTGAGACCATGAATCTATTTGCTGTGGTGGGCTGCTGCTCCATTTTTCACA 598  
Db 590 AAGCTGAGACCATGAATCTATTTGCTGTGGTGGGCTG-CTGCTGCATTTTTCACA 649  
Qy 599 CACTGAGCATCTGT 612  
Db 650 CACTGAGCATCTGT 663

RESULT 13  
LOCUS CD630067 682 bp mRNA linear EST 12-JAN-2004  
DEFINITION 5603908H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630067  
VERSION CD630067.1 GI:40278333  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Bukayocla; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com

## FEATURES

source 1..682  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 59.8%; Score 593.4; DB 6; Length 682;  
Best Local Similarity 97.2%; Pred. No. 3.1e-161;  
Matches 615; Conservative 0; Mismatches 16; Indels 2; Gaps 1;  
Qy 1 ATGGAACCAATGCGACCTTCAGCAATTAACAAGCAGAACTGCACAATTGAAAATCTTC 60  
Db 50 ATGGAACCAATGCGACCTTCAGCAATTAACAAGCAGAACTGCACAATTGAAAATCTTC 109  
Qy 61 AAGAGAGAAATTTTCCCAATGATATCGATTAATTTTTCGGGAGTCTTGGGAAT 120  
Db 110 AAGAGAGAAATTTTCCCAATGATATCGATTAATTTTTCGGGAGTCTTGGGAAT 169  
Qy 121 GGGTTGTCATATATGTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 180  
Db 170 GGGTTGTCATATATGTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 229  
Qy 181 AAGCTAAATCTGGCCATTCAGATCTCTGTTCAATAGACGCTTCCCTTCAAGGCTGAC 240

Db 230 ATGCTAAATCTGGCCATTTCAGATCTCTGTTCATTAAGACGGCTTCCTTCAGGGCTGAC 289  
Qy 241 TATTATCTTAAGAGCTCCCAATTGGATATTTGGAGACCTGGCTGCAGGATTAATGCTTAT 300  
Db 290 TATTATCTTAAGAGCTCCCAATTGGATATTTGGAGACCTGGCTGCAGGATTAATGCTTAT 349  
Qy 301 TCTTGTATGTAACATGATGACAGAGATTTATTTCTGACACCGTGTGAGTGTGAGCT 360  
Db 350 TCTTGTATGTAACATGATGACAGAGATTTATTTCTGACACCGTGTGAGTGTGAGCT 409  
Qy 361 TTCCTGGCAATGGTTCACCCCTTTGGCTTTCGATGTCATGTCACGACATCAGAGTGGCTGG 420  
Db 410 TTCCTGGCAATGGTTCACCCCTTTGGCTTTCGATGTCATGTCACGACATCAGAGTGGCTGG 469  
Qy 421 ATCTCTGTGGGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTCGACAGT 480  
Db 470 ATCTCTGTGGGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTCGACAGT 529  
Qy 481 GGCTGTGACAGACAGCGGAGTGTGACATGATGCTTATGAGCTGTAATCTTAATAA--TTG 538  
Db 530 GGCTGTGACAGACAGCGGAGTGTGACATGATGCTTATGAGCTGTAATCTTAATAAATTGC 589  
Qy 539 CTAACTGACAGACATGATTAATTCCTTGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598  
Db 590 CTAACTGACAGACATGATTAATTCCTTGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649  
Qy 599 CACTGACATCTGTTATCTGCTGATCATTCGGG 631  
Db 650 ACCTGACATCTGTTATCTGCTGATCATTCGGG 682

## RESULT 14

CF147785 729 bp mRNA linear EST 25-JUL-2003  
LOCUS AGENCOURT 14740183 NIH MGC 145 Homo sapiens cDNA clone  
DEFINITION IMAGE:6971946 5', mRNA sequence.  
ACCESSION CF147785  
VERSION CF147785.1 GI:33244053  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 729)  
NIH-MGC <http://mgi.mcl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRB102 row: f column: 05  
High quality sequence stop: 659.  
Location/Qualifiers

## FEATURES

Source 1..729  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6971946"  
/issue\_type="mixed"  
/lab\_host="DH108"  
/clone\_1lb="NIH MGC 145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XbaI/XhoI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
<ftp://image.llnl.gov/image/feared/plates/IRB1.presv.dat>  
a Note: this is a NIH\_MGC Library."

Query Match 56.9%; Score 565; DB 7; Length 729;  
Best Local Similarity 100.0%; Pred. No. 6e-153;  
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAACCAATGGACCTTCAGCATTAACAACAGACAGAACTGCACATTTGAAATCTTC 60  
Db 165 ATGGAACCAATGGACCTTCAGCATTAACAACAGACAGAACTGCACATTTGAAATCTTC 224  
Qy 61 AAGAGAAATTTTCCCAATGATATCTGATTAATTTTCTGGGAGCTTTGGAAAT 120  
Db 225 AAGAGAAATTTTCCCAATGATATCTGATTAATTTTCTGGGAGCTTTGGAAAT 284  
Qy 121 GGGTGTGCATATATGTTTCTCGACGCTTATAAGAACTCAACATCTGTAACGTTTTC 180  
Db 285 GGGTGTGCATATATGTTTCTCGACGCTTATAAGAACTCAACATCTGTAACGTTTTC 344  
Qy 181 ATGCTAAATCTGGCCATTTGAGATCTCGTTATATAGACGCTTCCCTTCAGGGCTGAC 240  
Db 345 ATGCTAAATCTGGCCATTTGAGATCTCGTTATATAGACGCTTCCCTTCAGGGCTGAC 404  
Qy 241 TATTATCTTAAGAGCTCCCAATTGGATATTTGGAGACCTGGCTGCAGGATTAATGCTTAT 300  
Db 405 TATTATCTTAAGAGCTCCCAATTGGATATTTGGAGACCTGGCTGCAGGATTAATGCTTAT 464  
Qy 301 TCTTGTATGTAACATGATGACAGAGATTTATTTCTGACACCGTGTGAGTGTGAGCT 360  
Db 465 TCTTGTATGTAACATGATGACAGAGATTTATTTCTGACACCGTGTGAGTGTGAGCT 524  
Qy 361 TTCCTGGCAATGGTTCACCCCTTTGGCTTTCGATGTCATGTCACGACATCAGAGTGGCTGG 420  
Db 525 TTCCTGGCAATGGTTCACCCCTTTGGCTTTCGATGTCATGTCACGACATCAGAGTGGCTGG 584  
Qy 421 ATCTCTGTGGGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTCGACAGT 480  
Db 585 ATCTCTGTGGGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTCGACAGT 644  
Qy 481 GGCTGTGACAGACAGCGGAGTGTGACATGATGCTTATGAGCTGTAATCTTAATAAATTGCT 540  
Db 645 GGCTGTGACAGACAGCGGAGTGTGACATGATGCTTATGAGCTGTAATCTTAATAAATTGCT 704  
Qy 541 AAGCTGACAGACCATGATCATTTTG 565  
Db 705 AAGCTGACAGACCATGATCATTTTG 729

## RESULT 15

CD630066 633 bp mRNA linear EST 12-JAN-2004  
LOCUS CD630066  
DEFINITION 56039816R6 Flp Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD630066  
VERSION CD630066.1 GI:40278332  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 633)  
Fu G.K., Wang J.T., Yang J., Au-Young J. and Stuve L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102



Email: [gfu@incyte.com](mailto:gfu@incyte.com).  
Location/Qualifiers  
1. .633

## ORIGIN

Query Match	54.7%	Score 543;	DB 6;	Length 633;
Best Local Similarity	99.8%;	Pred. No. 1.5e-146;		
Matches 554;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

OY	1	ATGAGCAAAATGGACCTTCAGCAATTAACAAGAGGAATGGACAATTGAAAATCTC	60
Db	50	ATGAGCAAAATGGACCTTCAGCAATTAACAAGAGGAATGGACAATTGAAAATCTC	105
OY	61	AAGAGAAATTTTCCCAATTGATATCTGATATATTTTCTGGGAGCTCTGGGAAAT	120
Db	110	AAGAGAAATTTTCCCAATTGATATCTGATATATTTTCTGGGAGCTCTGGGAAAT	165
OY	121	GGGTTGCCATATATGTTTTCTGCAGCCTTAAGAAGTCACATCTGGAAGCTTTC	180
Db	170	GGGTTGCCATATATGTTTTCTGCAGCCTTAAGAAGTCACATCTGGAAGCTTTC	225
OY	181	ATGCTAAATGGCCATTCCAGATCCCGTTCATATAGAGAGCTCCCTTAGAGGCTGAC	240
Db	230	ATGCTAAATGGCCATTCCAGATCCCGTTCATATAGAGAGCTCCCTTAGAGGCTGAC	285
OY	241	TATATCTTAGAGGCTCCAAATTGATATTTGGAGACTGGCTGCAGATATATCTTAT	300
Db	290	TATATCTTAGAGGCTCCAAATTGATATTTGGAGACTGGCTGCAGATATATCTTAT	345
OY	301	TCTTTGTAATCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGCGCT	360
Db	350	TCTTTGTAATCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGCGCT	405
OY	361	TTCTGTGCAATGGTTGACCCCTTTGGGCTTCGCATGTACACAGATCAAGAGTACGCTGG	420
Db	410	TTCTGTGCAATGGTTGACCCCTTTGGGCTTCGCATGTACACAGATCAAGAGTACGCTGG	465
OY	421	ATCCTCTGTGGATCATATGATATCCATTATCATAGCTTCTCCATAATATGCTCTTGAAGT	480
Db	470	ATCCTCTGTGGATCATATGATATCCATTATCATAGCTTCTCCATAATATGCTCTTGAAGT	525
OY	481	GGCTCTGAGCAGAACGGCAGTGTCAATCATGCTTTAGAGC-TGAATCTATAAAATTGC	539
Db	530	GGCTCTGAGCAGAACGGCAGTGTCAATCATGCTTTAGAGCTGAATCTATAAAATTGC	589
OY	540	TAACTGACAGCAAT 554	
Db	590	TAACTGACAGCAAT 604	

Search completed: March 20, 2005, 02:52:30  
Job time : 3872.5 secs



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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:53:02 ; Search time 44 Seconds  
(without alignments)  
721.626 Million cell updates/sec

Title: US-09-826-791a-2  
Perfect score: 1712  
Sequence: 1 MEPNCTFSNNNSRNCTIENF.....KAKTKCVFPVSVWLKRETRV 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%  
Maximum Match 100%  
Listing first 80 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Score	Match Length	ID	Description
-----				

No matches found

Search completed: April 1, 2005, 12:01:38  
Job time : 44 secs

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